

Db	121	AGGATATAGGCACATGGGCCACGCGGCTCTTTTAAACATTCGCCAGAGCTGTATCAGCCAA	180
OY	181	CCCATCTCACTGACATTTGGGAACTCCCCCCACGGCCATTACTGATCTGCGAGGTA	240
Db	181	CCCATCTCACTGCAATTTGGGAACTCCCCCCACGGCCATTACTGATCTGCGAGGTA	240
OY	241	AGACCAAGACACGAATGGGGGATTCACTCTAAGCTGTGGTGAAGGTGATGAAGAG	300
Db	241	AGACCAAGACACGAATGGGGGATTCACTCTAAGCTGTGGTGAAGGTGATGAAGAG	300
OY	301	AAGATCAGCGAAACAAAAGCCTCTAGGCTTTCTTACCAACAAACCTCTCTGCCCACCT	360
Db	301	AAGATCAGCGAAACAAAAGCCTCTAGGCTTTCTTACCAACAAACCTCTCTGCCCACCT	360
OY	361	GCTTTGAAAAGGGCGCAAGATATGTGGGGAAGCTGCCACCTGCTACAGTGAAGGATCT	420
Db	361	GCTTTGAAAAGGGCGCAAGATATGTGGGGAAGCTGCCACCTGCTACAGTGAAGGATCT	420
OY	421	GGAGAATFACTCACTTTGAGGTGCTCGCCCTTTCATCAGCCAGCTCTAACTTAAGCC	480
Db	421	GGAGAATFACTCACTTTGAGGTGCTCGCCCTTTCATCAGCCAGCTCTAACTTAAGCC	480
OY	481	AATGACCCCAAGGAGCTTACACAACTYCAAAAGGCCCAATGCAATTCATGACAGGGG	540
Db	481	AATGACCCCAAGGAGCTTACACAACTYCAAAAGGCCCAATGCAATTCATGACAGGGG	540
OY	541	GAGGCCAAAGGACTCCGGAGAGAGAGAGGCCCAATAAGGCTGGTGTATTTCCATTCATA	600
Db	541	GAGGCCAAAGGACTCCGGAGAGAGAGAGGCCCAATAAGGCTGGTGTATTTCCATTCATA	600
OY	601	GAGAGACAGAGGTGGCAAGCCCTTTTGATTATGTATCATTTGAAATGCAAGCTTCA	660
Db	601	GAGAGACAGAGGTGGCAAGCCCTTTTGATTATGTATCATTTGAAATGCAAGCTTCA	660
OY	661	AAATCCGGGTATCTCCGGGTGAGATAGAGAGACTTAAACCTCGGTGTGACAGGCAACCT	720
Db	661	AAATCCGGGTATCTCCGGGTGAGATAGAGAGACTTAAACCTCGGTGTGACAGGCAACCT	720
OY	721	CCAGGCGCGACTGGCCAGAGACAGATCCGCAAGAGGCTCTGAGCCAGCTCTGCTGCCAA	780
Db	721	CCAGGCGCGACTGGCCAGAGACAGATCCGCAAGAGGCTCTGAGCCAGCTCTGCTGCCAA	780
OY	781	GCCACTCGAATTTGAACCCCGGCTCTCTCAAGGTCAAGCTGTGTAGCTTGANTGAATCAAC	840
Db	781	GCCACTCGAATTTGAACCCCGGCTCTCTCAAGGTCAAGCTGTGTAGCTTGANTGAATCAAC	840
OY	841	TGCTATGACCAATCTGTCGCCAATTC	867
Db	841	TGCTATGACCAATCTGTCGCCAATTC	867

RESULT 2
US-09-969-730-12
; Sequence 12, Application US/09969730
; Publication No. US2003005443A1

1 TITLE OF INVENTION: 90 Human Secreted Proteins
2
3 FILE REFERENCE: P2013P
4
5 CURRENT APPLICATION NUMBER: US/09/969, 730
6
7 CURRENT FILING DATE: 2001-10-04
8
9 PRIOR APPLICATION NUMBER: 09/774,639
10
11 PRIOR FILING DATE: 2001-02-01
12
13 PRIOR APPLICATION NUMBER: 60/238,291
14
15 PRIOR FILING DATE: 2000-10-06
16
17 PRIOR APPLICATION NUMBER: 09/244,112
18
19 PRIOR FILING DATE: 1999-02-04
20
21 PRIOR APPLICATION NUMBER: PCT/US98/16235
22
23 PRIOR FILING DATE: 1998-08-04
24
25 PRIOR APPLICATION NUMBER: 60/056,371
26
27 PRIOR FILING DATE: 1997-08-19
28
29 PRIOR APPLICATION NUMBER: 60/056,732

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; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,367
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,365
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,731
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,557
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,563
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/055,970
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,986
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,311
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,808
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,803
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,809
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,806
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,310
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,798
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,309
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,312
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,807
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,386
; PRIOR FILING DATE: 1997-08-05
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 867
; TYPE: DNA
; ORGANISM: Homo sapiens
FEATURES:
; NAME/KEY: SITE
; LOCATION: (831)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-969-730-12
Query Match          99.8%; Score 865.2; DB 10; Length 867;
Match Local Similarity 100.0%; Pred. NO.6.9e-272;
Matches 867; Conservative 0; Mismatches 0; Gaps 0.

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Oy	TOAGTTTTTTTTTTTTTTTTTTTTTAAATGAGNAGGGGTTTCAACCGTGTACCGAGAT	60
Db	1 TOAGTTTTTTTTTTTTTTTTTTTTTAAATGAGNAGGGGTTTCAACCGTGTACCGAGAT	60
Oy	GGCTCGAATCTCTACCTCGTGAATCCGCCCGCGCTCCGACCTCCCAAGGCTGGATTAAC	120
Db	61 GGCTCGAATCTCTACCTCGTGAATCCGCCCGCGCTCCGACCTCCCAAGGCTGGATTAAC	120
Oy	GGTCTGAACTCTGACCTCTGATCGCCCGCGCTCCGACCTCCCAAGGCTGGATTAAC	180
Db	61 GGTCTGAACTCTGACCTCTGATCGCCCGCGCTCCGACCTCCCAAGGCTGGATTAAC	180
Oy	AGGCATGAGCACTGGCGCCACAGCGGTCTTTTAAATATCCCGAGACGTGTACAGCCAA	180
Db	121 AGGCATGAGCACTGGCGCCACAGCGGTCTTTTAAATATCCCGAGACGTGTACAGCCAA	180
Oy	AGGCATGAGCACTGGCGCCACAGCGGTCTTTTAAATATCCCGAGACGTGTACAGCCAA	180
Db	121 AGGCATGAGCACTGGCGCCACAGCGGTCTTTTAAATATCCCGAGACGTGTACAGCCAA	180

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QY 181 CCCATCTACCTGACATTTGGAACTCCCTCCCGAGGCACTAATGATTCGAGAGTA 240
DB 181 CCCATCTACCTGACATTTGGAACTCCCTCCCGAGGCACTAATGATTCGAGAGTA 240
QY 241 AGACCAAGAGCAAAATGGGGATTCACATTAAGGCTGGTATGATGATGAGGAG 300
DB 241 AGACCAAGAGCAAAATGGGGATTCACATTAAGGCTGGTATGATGATGAGGAG 300
QY 301 AAGATCAGCGAACTAAAGCTTTAGGCTTTTCTTACCAAAACCTCTCTGCCA 360
DB 301 AAGATCAGCGAACTAAAGCTTTAGGCTTTTCTTACCAAAACCTCTCTGCCA 360
QY 361 GCTTGAAGGGGAGAGATATAGTGGGAGAGGCTGCCAATCTCTCAAGAGGAGT 420
DB 361 GCTTGAAGGGGAGAGATATAGTGGGAGAGGCTGCCAATCTCTCAAGAGGAGT 420
QY 421 GGAATAATCTCACTTTAGGCTGCTGCTCTTCTTATGAGCAGCTTAAAGCC 480
DB 421 GGAATAATCTCACTTTAGGCTGCTGCTCTTCTTATGAGCAGCTTAAAGCC 480
QY 481 AATGACCCCAAGGAGCTTACAAATTCMAAGGCCAAATGCAATTCATGAGGAG 540
DB 481 AATGACCCCAAGGAGCTTACAAATTCMAAGGCCAAATGCAATTCATGAGGAG 540
QY 541 GAGGCCAAAGAGCTCCGAGAGAGAGGCCAATTAAGGCTGCTATTTCCGATCATA 600
DB 541 GAGGCCAAAGAGCTCCGAGAGAGAGGCCAATTAAGGCTGCTATTTCCGATCATA 600
QY 601 GAGAGAGCAGAGTGGGAGAGGCTTTTATATATATATTTTGAATGAGGAGTCA 660
DB 601 GAGAGAGCAGAGTGGGAGAGGCTTTTATATATATATTTTGAATGAGGAGTCA 660
QY 661 AATCCGAGGATATCCGAGGATGAGATGAGAGCTAAACCTGGTGTCAATGCAAGCT 720
DB 661 AATCCGAGGATATCCGAGGATGAGATGAGAGCTAAACCTGGTGTCAATGCAAGCT 720
QY 721 CCAAGGCGGAGCTGGCAGAGAGATCCGAGAGGCTTGAAGCAAGCTTGGTCCAA 780
DB 721 CCAAGGCGGAGCTGGCAGAGAGATCCGAGAGGCTTGAAGCAAGCTTGGTCCAA 780
QY 781 GGCACCTCGATTTGATGAGGCTGCTCTCAAGGCTCAAGTGTGATGATGATGAG 840
DB 781 GGCACCTCGATTTGATGAGGCTGCTCTCAAGGCTCAAGTGTGATGATGATGAG 840
QY 841 TGCTATGACCAATCTGCTGCGGAATTC 867
DB 841 TGCTATGACCAATCTGCTGCGGAATTC 867

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RESULT 3
US-10-621-363-12
; Sequence 12, Application us/10621363
; Publication No. US2004023283A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P2C1
; CURRENT APPLICATION NUMBER: US/10/621,363
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 09/969,730
; PRIOR FILING DATE: 2001-10-06
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19

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; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,370
; PRIOR FILING DATE: 1997-08-19
; Remaining Prior Application data removed - See File Wrapper or PAM.
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 12
; LENGTH: 867
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (831)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-621-363-12

Query Match
Best Local Similarity 100.0%; Pred. No. 6.9e-272; Length 867;
Matches 867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGAGTTTTTTTTTTTTTTTTTTTTTAAAGATGAGGATTTTACCGTTAGCCAGAT 60
DB 1 TCGAGTTTTTTTTTTTTTTTTTTTTTAAAGATGAGGATTTTACCGTTAGCCAGAT 60
QY 61 GGTCTGAACTCTGACCTCGATCCGCGGCTCGGCTCCCAAGTCTGGAGTAC 120
DB 61 GGTCTGAACTCTGACCTCGATCCGCGGCTCGGCTCCCAAGTCTGGAGTAC 120
QY 121 AGCAGTAGCCACTGCGCCGAGCCGCTTTTAAACATTTCCAGAGCTGAGCCCA 180
DB 121 AGCAGTAGCCACTGCGCCGAGCCGCTTTTAAACATTTCCAGAGCTGAGCCCA 180
QY 181 CCCATCTACCTGACATTTGGAACTCCCTCCCGAGGCACTAATGATTCGAGAGTA 240
DB 181 CCCATCTACCTGACATTTGGAACTCCCTCCCGAGGCACTAATGATTCGAGAGTA 240
QY 241 AGACCAAGAGCAAAATGGGGATTCACATTAAGGCTGGTATGATGATGAGGAG 300
DB 241 AGACCAAGAGCAAAATGGGGATTCACATTAAGGCTGGTATGATGATGAGGAG 300
QY 301 AAGATCAGCGAACTAAAGCTTTAGGCTTTTCTTACCAAAACCTCTCTGCCA 360
DB 301 AAGATCAGCGAACTAAAGCTTTAGGCTTTTCTTACCAAAACCTCTCTGCCA 360
QY 361 GCTTGAAGGGGAGAGATATAGTGGGAGAGGCTGCCAATCTCTCAAGAGGAGT 420
DB 361 GCTTGAAGGGGAGAGATATAGTGGGAGAGGCTGCCAATCTCTCAAGAGGAGT 420
QY 421 GGAATAATCTCACTTTAGGCTGCTGCTCTTCTTATGAGCAGCTTAAAGCC 480
DB 421 GGAATAATCTCACTTTAGGCTGCTGCTCTTCTTATGAGCAGCTTAAAGCC 480
QY 481 AATGACCCCAAGGAGCTTACAAATTCMAAGGCCAAATGCAATTCATGAGGAG 540
DB 481 AATGACCCCAAGGAGCTTACAAATTCMAAGGCCAAATGCAATTCATGAGGAG 540
QY 541 GAGGCCAAAGAGCTCCGAGAGAGAGGCCAATTAAGGCTGCTATTTCCGATCATA 600
DB 541 GAGGCCAAAGAGCTCCGAGAGAGAGGCCAATTAAGGCTGCTATTTCCGATCATA 600
QY 601 GAGAGAGCAGAGTGGGAGAGGCTTTTATATATATTTTGAATGAGGAGTCA 660
DB 601 GAGAGAGCAGAGTGGGAGAGGCTTTTATATATATTTTGAATGAGGAGTCA 660
QY 661 AATCCGAGGATATCCGAGGATGAGATGAGAGCTAAACCTGGTGTCAATGCAAGCT 720
DB 661 AATCCGAGGATATCCGAGGATGAGATGAGAGCTAAACCTGGTGTCAATGCAAGCT 720
QY 721 CCAAGGCGGAGCTGGCAGAGAGATCCGAGAGGCTTGAAGCAAGCTTGGTCCAA 780

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PRIORITY APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 51
LENGTH: 22255
TYPE: DNA
ORGANISM: Homo sapiens
US-10-671-242-51

Query Match      15.0%; Score 130.4; DB 13; Length 22255;
Best Local Similarity 89.7%; Pred. No. 5.le-31;
Matches 140; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 6 TTTTITTTTTTTTTTTTTTTAGTAGAGATGGGCTTCACCGGTGTAGCCAGATGCT 65
DB 7346 TTTTITTTTTTTTTTTTTTTAGTAGAGACGGGCTTCACCGGTGTAGCCAGATGCT 7405

QY 66 CGAATCTGTAAGCTCGTGATGCCCGCCTCGGCCTCCCAAATGCTGGATTACAGCA 125
DB 7406 CGATCTCTGTAAGCTCGTGATGCCCGCCTCGGCCTCCCAAATGCTGGATTACAGCT 7465

QY 126 TGAGCCACTGGCCAGCCGGCTCTTTTAAACATTC 161
DB 7466 TGAGCCACTGGCCAGCCGGCTCTTTTAAATTC 7501

RESULT 10
US-10-023-529-51
Sequence 51, Application US/10023529
Publication No. US2002012938BA1
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Aijona, Anibal A.
TITLE OR INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OR INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OR INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,529
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 51
LENGTH: 22255
TYPE: DNA
ORGANISM: Homo sapiens
US-10-023-529-51

Query Match      15.0%; Score 130.4; DB 14; Length 22255;
Best Local Similarity 89.7%; Pred. No. 5.le-31;
Matches 140; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 6 TTTTITTTTTTTTTTTTTTTAGTAGAGATGGGCTTCACCGGTGTAGCCAGATGCT 65
DB 7346 TTTTITTTTTTTTTTTTTTTAGTAGAGACGGGCTTCACCGGTGTAGCCAGATGCT 7405

QY 66 CGAATCTGTAAGCTCGTGATGCCCGCCTCGGCCTCCCAAATGCTGGATTACAGCA 125
DB 7406 CGATCTCTGTAAGCTCGTGATGCCCGCCTCGGCCTCCCAAATGCTGGATTACAGCT 7465

QY 126 TGAGCCACTGGCCAGCCGGCTCTTTTAAACATTC 161
DB 7466 TGAGCCACTGGCCAGCCGGCTCTTTTAAATTC 7501
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1	6	7.6	148567	4	US-09-801-976B-3	Sequence 3, Appl1
2	66	7.6	148567	4	US-10-924-869-3	Sequence 3, Appl1
3	64	7.4	460	4	US-08-918-686-26	Sequence 26, Appl1
4	64	7.4	819	3	US-09-337-171-13	Sequence 13, Appl1
5	4	7.4	819	4	US-09-773-459-13	Sequence 13, Appl1
6	64	7.4	92139	4	US-09-918-686-1	Sequence 1, Appl1
7	61	7.0	139806	4	US-09-740-028A-3	Sequence 1, Appl1
8	60	6.9	20966	4	US-07-776-576-7	Sequence 7, Appl1
9	60	6.9	20966	4	US-09-909-547-7	Sequence 7, Appl1
10	60	6.9	20966	4	US-09-569-652B-1	Sequence 1, Appl1
11	58	6.7	506	4	US-09-621-976-15373	Sequence 15373, A
12	58	6.7	92139	4	US-09-918-686-1	Sequence 1, Appl1
13	58	6.7	162450	4	US-08-335-882-1	Sequence 1, Appl1
14	57	6.6	495	4	US-09-653-976-11454	Sequence 11454, A
15	57	6.6	20598	4	US-05-553-995-10	Sequence 10, Appl1
16	55	6.5	13158	2	US-08-687-080-105	Sequence 105, A
17	55	6.3	203	4	US-09-621-976-10774	Sequence 10774, A
18	55	6.3	260	4	US-09-621-976-10668	Sequence 10668, A
19	55	6.3	288	1	US-08-157-171-8	Sequence 8, Appl1
20	55	6.3	289	4	US-09-621-976-10116	Sequence 10116, A
21	55	6.3	293	4	US-09-621-976-10356	Sequence 10356, A
22	55	6.3	293	4	US-09-621-976-10404	Sequence 10404, A
23	55	6.3	293	4	US-09-621-976-11002	Sequence 11002, A
24	55	6.3	293	4	US-09-621-976-11159	Sequence 11159, A
25	55	6.3	293	4	US-09-621-976-13512	Sequence 13512, A
26	55	6.3	302	4	US-09-621-976-12511	Sequence 12511, A
27	55	6.3	303	4	US-09-621-976-9840	Sequence 9840, A

NUMBER OF SEQ ID NOS: 8

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 148567
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(148567)
OTHER INFORMATION: n = A,T,C or G
US-10-254-869-3

Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e-20; Length 148567;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 CTCCTGACCTCGTATCCGCCCTCGGCTCCCAAGTCTGGATTACAGGCATGAG 129
DB 81514 CTCCTGACCTCGTATCCGCCCTCGGCTCCCAAGTCTGGATTACAGGCATGAG 81573
QY 130 CCAC 135
DB 81574 CCAC 81579

RESULT 3
US-09-918-686-26
Sequence 26, Application US/09918686
Patent No. 6475739
GENERAL INFORMATION:
APPLICANT: Brunkow, Mary
APPLICANT: Prohl, Sean
APPLICANT: Paepfer, Bryan
APPLICANT: Staehling-Hampton, Karen
TITLE OF INVENTION: METHODS FOR IDENTIFYING
TITLE OF INVENTION: GENOMIC DELETIONS
FILE REFERENCE: 240083.515
CURRENT APPLICATION NUMBER: US/09/918.686
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26
LENGTH: 460
TYPE: DNA
ORGANISM: Homo sapiens
US-09-918-686-26

Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-19; Length 460;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 CTCCTGACCTCGTATCCGCCCTCGGCTCCCAAGTCTGGATTACAGGCATGAG 129
DB 316 CTCCTGACCTCGTATCCGCCCTCGGCTCCCAAGTCTGGATTACAGGCATGAG 375
QY 130 CCAC 133
DB 376 CCAC 379

RESULT 4
US-09-337-171-13/c
Sequence 13, Application US/09337171
Patent No. 6262249
GENERAL INFORMATION:
APPLICANT: Kennedy, Giulia C
APPLICANT: Paepfer, Bryan
APPLICANT: Staehling-Hampton, Karen
TITLE OF INVENTION: PANCREATIC CANCER GENES
FILE REFERENCE: 200130.454
CURRENT APPLICATION NUMBER: US/09/337.171
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 13
LENGTH: 819

TYPE: DNA
ORGANISM: Homo sapien
US-09-337-171-13

Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-19; Length 819;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 CTCCTGACCTCGTATCCGCCCTCGGCTCCCAAGTCTGGATTACAGGCATGAG 129
DB 769 CTCCTGACCTCGTATCCGCCCTCGGCTCCCAAGTCTGGATTACAGGCATGAG 710
QY 130 CCAC 133
DB 709 CCAC 706

RESULT 5
US-09-773-459-13/c
Sequence 13, Application US/09773459
Patent No. 664054
GENERAL INFORMATION:
APPLICANT: Kennedy, Giulia C
APPLICANT: Paepfer, Bryan
APPLICANT: Staehling-Hampton, Karen
TITLE OF INVENTION: PANCREATIC CANCER GENES
FILE REFERENCE: 200130.454
CURRENT APPLICATION NUMBER: US/09/773.459
CURRENT FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: US 09/337.171
PRIOR FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 13
LENGTH: 819
TYPE: DNA
ORGANISM: Homo sapien
US-09-773-459-13

Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e-19; Length 819;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 CTCCTGACCTCGTATCCGCCCTCGGCTCCCAAGTCTGGATTACAGGCATGAG 129
DB 769 CTCCTGACCTCGTATCCGCCCTCGGCTCCCAAGTCTGGATTACAGGCATGAG 710
QY 130 CCAC 133
DB 709 CCAC 706

RESULT 6
US-09-918-686-1
Sequence 1, Application US/09918686
Patent No. 6475739
GENERAL INFORMATION:
APPLICANT: Brunkow, Mary
APPLICANT: Prohl, Sean
APPLICANT: Paepfer, Bryan
APPLICANT: Staehling-Hampton, Karen
TITLE OF INVENTION: METHODS FOR IDENTIFYING
TITLE OF INVENTION: GENOMIC DELETIONS
FILE REFERENCE: 240083.515
CURRENT APPLICATION NUMBER: US/09/918.686
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 92139
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 7043, 8369, 8401

OTHER INFORMATION: n = A,T,C or G
US-09-918-686-1

Query Match 7.4%; Score 64; DB 4; Length 92139;
Best Local Similarity 100.0%; Pred. No. 9.4e-20;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 CTCCTGACCTCGTATCGCGCCCTCGGCTCCCAAGTGTGGATTACAGGATGAG 129
DB 2380 CTCCTGACCTCGTATCGCGCCCTCGGCTCCCAAGTGTGGATTACAGGATGAG 2439
QY 130 CCAC 133
DB 2440 CCAC 2443

RESULT 7
US-09-740-028A-3
Sequence 3, Application US/09740028A
Patent No. 6410289

GENERAL INFORMATION:
APPLICANT: GONG, Fangcheng et al
TITLE OF INVENTION: ISOLATED HUMAN DEHYDROGENASES, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING THESE HUMAN DEHYDROGENASES, AND USES
FILE REFERENCE: C1001054
CURRENT APPLICATION NUMBER: US/09/740,028A
CURRENT FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 19806
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(19806)
OTHER INFORMATION: n = A,T,C or G
US-09-740-028A-3

Query Match 7.0%; Score 61; DB 4; Length 19806;
Best Local Similarity 100.0%; Pred. No. 2.3e-18;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 TGGTCTGCACTCTGACCTCGTATCGCGCCCTCGGCTCCCAAGTGTGGATTG 119
DB 266 TGGTCTGCACTCTGACCTCGTATCGCGCCCTCGGCTCCCAAGTGTGGATTG 325
QY 120 C 120
DB 326 C 326

RESULT 8
US-09-776-976-7/c
Sequence 7, Application US/09776976
Patent No. 6566332
GENERAL INFORMATION:
APPLICANT: Truebis, Joachim
APPLICANT: Erickson, Mary Ruth
APPLICANT: Yen, Frances
APPLICANT: Bihain, Bernard
TITLE OF INVENTION: OB63 Globular Head and Uses Thereof for Decreasing Body Mass
FILE REFERENCE: 76.USA.REG
CURRENT APPLICATION NUMBER: US/09/776,976
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/758,055
PRIOR FILING DATE: 2001-01-10
PRIOR APPLICATION NUMBER: US 60/176,228
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/198,087
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: US 60/299,881

PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent.pm
SEQ ID NO 7
LENGTH: 20966
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..4811
OTHER INFORMATION: 5' regulatory region
NAME/KEY: exon
LOCATION: 4812..4851
OTHER INFORMATION: exon 1
NAME/KEY: exon
LOCATION: 15144..15365
OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 16277..20559
OTHER INFORMATION: exon 3
NAME/KEY: misc_feature
LOCATION: 20560..20966
OTHER INFORMATION: 3' regulatory region
NAME/KEY: allele
LOCATION: 3787
OTHER INFORMATION: 9-27-261 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 1118
OTHER INFORMATION: 99-14387-129 : polymorphic base A or C
NAME/KEY: allele
LOCATION: 15120
OTHER INFORMATION: 9-12-48 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 15196
OTHER INFORMATION: 9-12-124 : polymorphic base G or T
NAME/KEY: allele
LOCATION: 15427
OTHER INFORMATION: 9-12-355 : polymorphic base G or T
NAME/KEY: allele
LOCATION: 15500
OTHER INFORMATION: 9-12-428 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 15863
OTHER INFORMATION: 99-14405-105 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 17170
OTHER INFORMATION: 9-16-189 : polymorphic base deletion of A
NAME/KEY: primer_bind
LOCATION: 3528..3545
OTHER INFORMATION: 9-27.pu
NAME/KEY: primer_bind
LOCATION: 3928..3946
OTHER INFORMATION: 9-27..rp complement
NAME/KEY: primer_bind
LOCATION: 10990..11008
OTHER INFORMATION: 99-14387.pu
NAME/KEY: primer_bind
LOCATION: 11423..11442
OTHER INFORMATION: 99-14387..rp complement
NAME/KEY: primer_bind
LOCATION: 15073..15092
OTHER INFORMATION: 9-12.pu
NAME/KEY: primer_bind
LOCATION: 15503..15520
OTHER INFORMATION: 9-12..rp complement
NAME/KEY: primer_bind
LOCATION: 15759..15776
OTHER INFORMATION: 99-14405.pu
NAME/KEY: primer_bind
LOCATION: 16181..16211
OTHER INFORMATION: 99-14405..rp complement
NAME/KEY: primer_bind
LOCATION: 16982..17001

OTHER INFORMATION: 9-16.pu
 NAME/KEY: primer bind
 LOCATION: 17384..17402
 OTHER INFORMATION: 9-16-tp complement
 NAME/KEY: misc binding
 LOCATION: 3775..3799
 OTHER INFORMATION: 9-27-261.probe
 NAME/KEY: misc binding
 LOCATION: 11106..11130
 OTHER INFORMATION: 99-14387-129.probe
 NAME/KEY: misc binding
 LOCATION: 15108..15132
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 NAME/KEY: misc binding
 LOCATION: 15184..15208
 OTHER INFORMATION: 9-12-124.probe
 NAME/KEY: misc binding
 LOCATION: 15415..15439
 OTHER INFORMATION: 9-12-355.probe
 NAME/KEY: misc binding
 LOCATION: 15485..15512
 OTHER INFORMATION: 9-12-428.probe
 NAME/KEY: misc binding
 LOCATION: 15851..15875
 OTHER INFORMATION: 99-14405-105.probe
 NAME/KEY: misc binding
 LOCATION: 17158..17182
 OTHER INFORMATION: 9-16-189.probe
 NAME/KEY: primer bind
 LOCATION: 3768..3786
 OTHER INFORMATION: 9-27-261.mis
 NAME/KEY: primer bind
 LOCATION: 3788..3806
 OTHER INFORMATION: 9-27-261.mis complement
 NAME/KEY: primer bind
 LOCATION: 11099..11117
 OTHER INFORMATION: 99-14387-129.mis
 NAME/KEY: primer bind
 LOCATION: 11119..11137
 OTHER INFORMATION: 99-14387-129.mis complement
 NAME/KEY: primer bind
 LOCATION: 15101..15119
 OTHER INFORMATION: 9-12-48.mis
 NAME/KEY: primer bind
 LOCATION: 15121..15139
 OTHER INFORMATION: 9-12-48.mis complement
 NAME/KEY: primer bind
 LOCATION: 15177..15195
 OTHER INFORMATION: 9-12-124.mis
 NAME/KEY: primer bind
 LOCATION: 15197..15215
 OTHER INFORMATION: 9-12-124.mis complement
 NAME/KEY: primer bind
 LOCATION: 15408..15426
 OTHER INFORMATION: 9-12-355.mis
 NAME/KEY: primer bind
 LOCATION: 15428..15446
 OTHER INFORMATION: 9-12-355.mis complement
 NAME/KEY: primer bind
 LOCATION: 15481..15499
 OTHER INFORMATION: 9-12-428.mis
 NAME/KEY: primer bind
 LOCATION: 15501..15519
 OTHER INFORMATION: 9-12-428.mis complement
 NAME/KEY: primer bind
 LOCATION: 15844..15862
 OTHER INFORMATION: 99-14405-105.mis
 NAME/KEY: primer bind
 LOCATION: 15864..15882
 OTHER INFORMATION: 99-14405-105.mis complement
 NAME/KEY: primer bind
 LOCATION: 17151..17169
 OTHER INFORMATION: 9-16-189.mis

NAME/KEY: primer bind
 LOCATION: 17171..17189
 OTHER INFORMATION: 9-16-189.mis complement
 US-09-776-976-7
 Query Match 6.9%; Score 60; DB 4; Length 20966;
 Best Local Similarity 100.0%; Pred.No. 6,5e-18;
 Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 81 GTGATCGCCCGCCCTCGCCCTCCCAAGTCTGGATTACAGCATTGAGCCCTGCGCC 140
 Db 10046 GTGATCGCCCGCCCTCGCCCTCCCAAGTCTGGATTACAGCATTGAGCCCTGCGCC 9987
 RESULT 9
 US-09-909-547-7/C
 Sequence 7, Application US/0909547
 Patent No. 6579852
 GENERAL INFORMATION:
 APPLICANT: Fruebis, Joachim
 APPLICANT: Erickson, Mary Ruth
 APPLICANT: Yen, Frances
 APPLICANT: Bihain, Bernard
 TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
 FILE REFERENCE: 76.US6.CIP
 CURRENT APPLICATION NUMBER: US/09/909,547
 CURRENT FILING DATE: 2001-07-19
 PRIOR APPLICATION NUMBER: US 09/776,976
 PRIOR FILING DATE: 2001-02-05
 PRIOR APPLICATION NUMBER: US 09/758,055
 PRIOR FILING DATE: 2001-01-10
 PRIOR APPLICATION NUMBER: US 60/299,881
 PRIOR FILING DATE: 2000-09-01
 PRIOR APPLICATION NUMBER: US 60/198,087
 PRIOR FILING DATE: 2000-04-13
 PRIOR APPLICATION NUMBER: US 60/176,228
 PRIOR FILING DATE: 2000-01-14
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: Patent.pm
 SEQ ID NO 7
 LENGTH: 20966
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: 1..4811
 OTHER INFORMATION: 5' regulatory region
 NAME/KEY: exon
 LOCATION: 4812..4851
 OTHER INFORMATION: exon 1
 NAME/KEY: exon
 LOCATION: 15144..15365
 OTHER INFORMATION: exon 2
 NAME/KEY: exon
 LOCATION: 16277..20559
 OTHER INFORMATION: exon 3
 NAME/KEY: misc feature
 LOCATION: 20560..20966
 OTHER INFORMATION: 3' regulatory region
 NAME/KEY: allele
 LOCATION: 3787
 OTHER INFORMATION: 9-27-261 : polymorphic base G or C
 NAME/KEY: allele
 LOCATION: 11118
 OTHER INFORMATION: 99-14387-129 : polymorphic base A or C
 NAME/KEY: allele
 LOCATION: 15120
 OTHER INFORMATION: 9-12-48 : polymorphic base C or T
 NAME/KEY: allele
 LOCATION: 15196
 OTHER INFORMATION: 9-12-124 : polymorphic base G or T
 NAME/KEY: allele
 LOCATION: 15427

OTHER INFORMATION: 9-12-355 : polymorphic base G or T
NAME/KEY: allele
LOCATION: 15500
OTHER INFORMATION: 9-12-428 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 15863
OTHER INFORMATION: 9-14405-105 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 17170
OTHER INFORMATION: 9-16-189 : polymorphic base deletion of A
NAME/KEY: primer_bind
LOCATION: 3528..3545
OTHER INFORMATION: 9-27-pu
NAME/KEY: primer_bind
LOCATION: 3928..3946
OTHER INFORMATION: 9-27-rp complement
NAME/KEY: primer_bind
LOCATION: 10990..11008
OTHER INFORMATION: 9-14387-pu
NAME/KEY: primer_bind
LOCATION: 11423..11442
OTHER INFORMATION: 9-14387-rp complement
NAME/KEY: primer_bind
LOCATION: 15073..15092
OTHER INFORMATION: 9-12-pu
NAME/KEY: primer_bind
LOCATION: 15503..15520
OTHER INFORMATION: 9-12-rp complement
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LOCATION: 15759..15776
OTHER INFORMATION: 9-14405-pu
NAME/KEY: primer_bind
LOCATION: 16191..16211
OTHER INFORMATION: 9-14405-rp complement
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LOCATION: 16982..17001
OTHER INFORMATION: 9-16-pu
NAME/KEY: primer_bind
LOCATION: 17384..17402
OTHER INFORMATION: 9-16-rp complement
NAME/KEY: misc_binding
LOCATION: 3775..3799
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NAME/KEY: misc_binding
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NAME/KEY: misc_binding
LOCATION: 15108..15132
OTHER INFORMATION: 9-12-48-probe
NAME/KEY: misc_binding
LOCATION: 15184..15208
OTHER INFORMATION: 9-12-124-probe
NAME/KEY: misc_binding
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OTHER INFORMATION: 9-12-355-probe
NAME/KEY: misc_binding
LOCATION: 15488..15512
OTHER INFORMATION: 9-12-428-probe
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OTHER INFORMATION: 9-14405-105-probe
NAME/KEY: misc_binding
LOCATION: 17158..17182
OTHER INFORMATION: 9-16-189-probe
NAME/KEY: primer_bind
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NAME/KEY: primer_bind
LOCATION: 3788..3806
OTHER INFORMATION: 9-27-261-mis complement
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LOCATION: 11099..11117
OTHER INFORMATION: 9-14387-129-mis

NAME/KEY: primer_bind
LOCATION: 11119..11137
OTHER INFORMATION: 9-14387-129-mis complement
NAME/KEY: primer_bind
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OTHER INFORMATION: 9-12-48-mis
NAME/KEY: primer_bind
LOCATION: 15121..15139
OTHER INFORMATION: 9-12-48-mis complement
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OTHER INFORMATION: 9-12-124-mis
NAME/KEY: primer_bind
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OTHER INFORMATION: 9-12-124-mis complement
NAME/KEY: primer_bind
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NAME/KEY: primer_bind
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OTHER INFORMATION: 9-12-355-mis complement
NAME/KEY: primer_bind
LOCATION: 15481..15499
OTHER INFORMATION: 9-12-428-mis
NAME/KEY: primer_bind
LOCATION: 15501..15519
OTHER INFORMATION: 9-12-428-mis complement
NAME/KEY: primer_bind
LOCATION: 15844..15862
OTHER INFORMATION: 9-14405-105-mis
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OTHER INFORMATION: 9-14405-105-mis complement
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LOCATION: 17151..17169
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NAME/KEY: primer_bind
LOCATION: 17171..17189
OTHER INFORMATION: 9-16-189-mis complement
US-09-909-547-7

Query Match 6.9%; Score 60; DB 4; Length 20966;
Best Local Similarity 100.0%; Pred. No. 6,5e-18;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 GTGATCGCCGCGCTCCCAAGTGTGAGTACAGGATGACCGACCGGCC 140
DB 10046 GTGATCGCCGCGCTCCCAAGTGTGAGTACAGGATGACCGACCGGCC 9987

US-09-569-8528-1/c
Sequence 1, Application US/095698528
Patent No. 6582909
GENERAL INFORMATION:
APPLICANT: Bouquelerc, Lydie
APPLICANT: Bihain, Bernard
APPLICANT: Denison, Blake
TITLE OF INVENTION: APM1 Biallelic Markers and Uses Thereof
FILE REFERENCE: GEN-T113KC2
CURRENT APPLICATION NUMBER: US/09/569,8528
PRIORITY FILING DATE: 2002-03-12
PRIORITY APPLICATION NUMBER: PCT/IB99/01858
PRIORITY FILING DATE: 1999-11-04
PRIORITY APPLICATION NUMBER: US 09/434,848
PRIORITY FILING DATE: 1999-11-04
PRIORITY APPLICATION NUMBER: US 60/119,593
PRIORITY FILING DATE: 1999-02-10
PRIORITY APPLICATION NUMBER: US 60/107,113
PRIORITY FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1

Fri May 28 12:50:56 2004

us-10-621-363-12.rn1

Page 6

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SEQ ID NO 1
LENGTH: 20966
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(4811)
OTHER INFORMATION: 5' regulatory region
NAME/KEY: primer_bind
LOCATION: (14683)..(14701)
OTHER INFORMATION: 17-34-860.mis
NAME/KEY: primer_bind
LOCATION: (14703)..(14721)
OTHER INFORMATION: 17-34-860.mis complement
NAME/KEY: primer_bind
LOCATION: (14738)..(14756)
OTHER INFORMATION: 17-34-915.mis
NAME/KEY: primer_bind
LOCATION: (14758)..(14776)
OTHER INFORMATION: 17-34-915.mis complement
NAME/KEY: primer_bind
LOCATION: (14796)..(14814)
OTHER INFORMATION: 17-35-71.mis
NAME/KEY: primer_bind
LOCATION: (14816)..(14834)
OTHER INFORMATION: 17-35-71.mis complement
NAME/KEY: primer_bind
LOCATION: (15031)..(15049)
OTHER INFORMATION: 17-35-306.mis
NAME/KEY: primer_bind
LOCATION: (15051)..(15069)
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NAME/KEY: primer_bind
LOCATION: (15121)..(15139)
OTHER INFORMATION: 9-12-48.mis complement
NAME/KEY: primer_bind
LOCATION: (15177)..(15195)
OTHER INFORMATION: 9-12-124.mis
NAME/KEY: primer_bind
LOCATION: (15197)..(15215)
OTHER INFORMATION: 9-12-124.mis complement
NAME/KEY: primer_bind
LOCATION: (15408)..(15426)
OTHER INFORMATION: 9-12-355.mis
NAME/KEY: primer_bind
LOCATION: (15428)..(15446)
OTHER INFORMATION: 9-12-355.mis complement
NAME/KEY: primer_bind
LOCATION: (15481)..(15499)
OTHER INFORMATION: 9-12-428.mis
NAME/KEY: primer_bind
LOCATION: (15501)..(15519)
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NAME/KEY: primer_bind
LOCATION: (15661)..(15679)
OTHER INFORMATION: 17-36-47.mis
NAME/KEY: primer_bind
LOCATION: (15681)..(15699)
OTHER INFORMATION: 17-36-47.mis complement
NAME/KEY: primer_bind
LOCATION: (15771)..(15789)
OTHER INFORMATION: 17-36-120.mis
NAME/KEY: primer_bind
LOCATION: (15791)..(15809)
OTHER INFORMATION: 17-36-120.mis complement
NAME/KEY: primer_bind
LOCATION: (15846)..(15862)
OTHER INFORMATION: 99-14405-105.mis
NAME/KEY: primer_bind
LOCATION: (15864)..(15882)
OTHER INFORMATION: 99-14405-105.mis complement
NAME/KEY: primer_bind
LOCATION: (17151)..(17169)
OTHER INFORMATION: 9-16-189.mis
NAME/KEY: primer_bind
LOCATION: (17171)..(17189)
OTHER INFORMATION: 9-16-189.mis complement
NAME/KEY: primer_bind
LOCATION: (17816)..(17828)
OTHER INFORMATION: 17-37-629.mis
NAME/KEY: primer_bind
LOCATION: (17830)..(17848)
OTHER INFORMATION: 17-37-629.mis complement
NAME/KEY: primer_bind
LOCATION: (17992)..(18010)
OTHER INFORMATION: 17-37-811.mis
NAME/KEY: primer_bind
LOCATION: (18012)..(18030)
OTHER INFORMATION: 17-38-349.mis
NAME/KEY: primer_bind
LOCATION: (18470)..(18488)
OTHER INFORMATION: 17-38-349.mis complement
NAME/KEY: primer_bind
LOCATION: (18490)..(18508)
OTHER INFORMATION: 17-30-216.mis
NAME/KEY: primer_bind
LOCATION: (1926)..(1944)
OTHER INFORMATION: 17-30-216.mis complement
NAME/KEY: primer_bind
LOCATION: (1946)..(1964)
OTHER INFORMATION: 17-30-216.mis complement
NAME/KEY: primer_bind
LOCATION: (3719)..(3737)
OTHER INFORMATION: 9-27-211.mis
NAME/KEY: primer_bind
LOCATION: (3739)..(3757)
OTHER INFORMATION: 9-27-211.mis complement
NAME/KEY: primer_bind
LOCATION: (3754)..(3772)
OTHER INFORMATION: 9-27-246.mis
NAME/KEY: primer_bind
LOCATION: (3774)..(3792)
OTHER INFORMATION: 9-27-246.mis complement
NAME/KEY: primer_bind
LOCATION: (3768)..(3786)
OTHER INFORMATION: 9-27-261.mis
NAME/KEY: primer_bind
LOCATION: (3788)..(3806)
OTHER INFORMATION: 9-27-261.mis complement
NAME/KEY: primer_bind
LOCATION: (5076)..(5094)
OTHER INFORMATION: 17-31-298.mis
NAME/KEY: primer_bind
LOCATION: (5096)..(5114)
OTHER INFORMATION: 17-31-298.mis complement
NAME/KEY: primer_bind
LOCATION: (5191)..(5209)
OTHER INFORMATION: 17-31-413.mis
NAME/KEY: primer_bind
LOCATION: (5211)..(5229)
OTHER INFORMATION: 17-31-413.mis complement
NAME/KEY: primer_bind
LOCATION: (5364)..(5382)
OTHER INFORMATION: 17-31-413.mis complement
NAME/KEY: primer_bind
LOCATION: (10618)..(10636)
OTHER INFORMATION: 17-32-24.mis
NAME/KEY: primer_bind
LOCATION: (10638)..(10656)
OTHER INFORMATION: 17-32-24.mis complement
NAME/KEY: primer_bind
LOCATION: (11020)..(11038)
OTHER INFORMATION: 99-14387-50.mis
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NAME/KEY: primer bind
LOCATION: (11040)..(11058)
OTHER INFORMATION: 99-14387-50. mis complement
NAME/KEY: primer bind
LOCATION: (11099)..(11117)
OTHER INFORMATION: 99-14387-129. mis
NAME/KEY: primer bind
LOCATION: (11119)..(11137)
OTHER INFORMATION: 99-14387-129. mis complement
NAME/KEY: primer bind
LOCATION: (11169)..(11187)
OTHER INFORMATION: 99-14387-199. mis
NAME/KEY: primer bind
LOCATION: (11189)..(11207)
OTHER INFORMATION: 99-14387-199. mis complement
NAME/KEY: primer bind
LOCATION: (13954)..(13972)
OTHER INFORMATION: 17-33-TGAGACT.mis
NAME/KEY: primer bind
LOCATION: (13974)..(13992)
OTHER INFORMATION: 17-33-TGAGACT.mis complement
NAME/KEY: exon
LOCATION: (4812)..(4851)
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (15144)..(15365)
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (16277)..(20559)
OTHER INFORMATION:
NAME/KEY: misc feature
LOCATION: (20560)..(20966)
OTHER INFORMATION: 3' regulatory region

Query Match 6.9%; Score 60; DB 4; Length 20966;
Best Local Similarity 100.0%; Pred. No. 6.5e-18;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

81 GTGATCCGCCCGCTCCGCTCCCAAGTCTGGATTACAGGCATGAGCCACTGGCC 140
10046 GTGATCCGCCCGCTCCGCTCCCAAGTCTGGATTACAGGCATGAGCCACTGGCC 9987

RESULT 11
US-09-621-976-15373
Sequence 15373, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621.976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 15373
LENGTH: 506
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-15373

Query Match 6.7%; Score 58; DB 4; Length 506;
Best Local Similarity 100.0%; Pred. No. 6.6e-17;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

76 ACCTCGATCCGCTCCGCTCCCAAGTCTGGATTACAGGCATGAGCCAC 133
51 ACCTCGATCCGCTCCGCTCCCAAGTCTGGATTACAGGCATGAGCCAC 108

RESULT 12

US-09-918-686-1/c
Sequence 1, Application US/09918686
Patent No. 645739
GENERAL INFORMATION:
APPLICANT: Brunkow, Mary
APPLICANT: Prohl, Sean
APPLICANT: Paepfer, Bryan
APPLICANT: Staehling-Hampton, Karen
TITLE OF INVENTION: METHODS FOR IDENTIFYING
TITLE OF INVENTION: GENOMIC DELETIONS
FILE REFERENCE: 240083.515
CURRENT APPLICATION NUMBER: US/09/918.686
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 92139
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 7043, 8369, 8401
OTHER INFORMATION: n = A,T,C or G
US-09-918-686-1

Query Match 6.7%; Score 58; DB 4; Length 92139;
Best Local Similarity 100.0%; Pred. No. 4.8e-17;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

81 GTGATCCGCCCGCTCCGCTCCCAAGTCTGGATTACAGGCATGAGCCACTGGCC 138
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RESULT 13
US-09-345-882-1
Sequence 1, Application US/09345882
Patent No. 6398373
GENERAL INFORMATION:
APPLICANT: Bouguetelret, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
FILE REFERENCE: GENSET.031A
CURRENT APPLICATION NUMBER: US/09/345.882
CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: US 60/091.315
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/111.909
PRIOR FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 140
SOFTWARE: Patent.pm
SEQ ID NO 1
LENGTH: 16250
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 72794
OTHER INFORMATION: 5-124-273 : polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 88073
OTHER INFORMATION: 5-127-261 : polymorphic base A or C
FEATURE:
NAME/KEY: allele
LOCATION: 90842
OTHER INFORMATION: 99-1437-325 : polymorphic base A or G

FEATURE:
NAME/KEY: allele
LOCATION: 93714
OTHER INFORMATION: 5-128-60 : polymorphic base deletion of GT
FEATURE:
NAME/KEY: allele

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1 OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
2 FEATURE:
3 NAME/KEY: allele
4 LOCATION: 88050..88096
5 OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID51
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8 LOCATION: 88050..88096
9 OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
10 FEATURE:
11 NAME/KEY: allele
12 LOCATION: 90819..90865
13 OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
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15 NAME/KEY: allele
16 LOCATION: 90819..90865
17 OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
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20 LOCATION: 93690..93736
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22 FEATURE:
23 NAME/KEY: allele
24 LOCATION: 93690..93736
25 OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
26 FEATURE:
27 NAME/KEY: allele
28 LOCATION: 97099..97145
29 OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
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31 NAME/KEY: allele
32 LOCATION: 97130..97177
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47 NAME/KEY: allele
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49 OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
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51 NAME/KEY: allele
52 LOCATION: 99094..99140
53 OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
54 FEATURE:
55 NAME/KEY: allele
56 LOCATION: 103783..103828
57 OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
58 FEATURE:
59 NAME/KEY: allele
60 LOCATION: 103783..103828
61 OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
62 FEATURE:
63 NAME/KEY: allele
64 LOCATION: 106918..106966
65 OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
66 FEATURE:
67 NAME/KEY: allele
68 LOCATION: 106918..106966
69 OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
70

```

```

; FEATURE:
; NAME/KEY: allele
; LOCATION: 108084..108130
; OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
; FEATURE:
; NAME/KEY: allele
; LOCATION: 108084..108130
; OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
; FEATURE:
; NAME/KEY: allele
; LOCATION: 108127..108177
; OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
; FEATURE:
; NAME/KEY: allele
; LOCATION: 108127..108177
; OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
; FEATURE:

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Query Match          6.7%; Score 58; DB 4; Length 162450;
Best Local Similarity 100.0%; Pred. No. 4.6e-17;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      82 TGATCCGCGCGCTCGGCTCCCAAGTGTGGATTACAGGATGACCTGCGCC 139
DB      153473 TGATCCGCGCGCTCGGCTCCCAAGTGTGGATTACAGGATGACCTGCGCC 153530

```

```

RESULT 14
US-09-621-976-11454/c
; Sequence 11454, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Uobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 11454
; LENGTH: 495
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 489
; OTHER INFORMATION: n=a, g, c o r t
US-09-621-976-11454

```

```

Query Match          6.6%; Score 57; DB 4; Length 495;
Best Local Similarity 100.0%; Pred. No. 1.9e-16;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      68 AACTCTGACCTCGTATCGCCGCGCTCGGCTCCCAAGTGTGGATTACAGGC 124
DB      94 AACTCTGACCTCGTATCGCCGCGCTCGGCTCCCAAGTGTGGATTACAGGC 38

```

```

RESULT 15
US-09-593-995-10/c
; Sequence 10, Application US/09593995
; Patent No. 6406888
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: HELICAL CYTOKINE ZALPHA33
; FILE REFERENCE: 99-38
; CURRENT APPLICATION NUMBER: US/09/593,995
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 60/139,121
; PRIOR FILING DATE: 1999-06-14

```

```

; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 20598
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-593-995-10

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```

Query Match          6.6%; Score 57; DB 4; Length 20598;
Best Local Similarity 100.0%; Pred. No. 1.5e-16;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      70 CTCTGACCTCGTATCGCCGCGCTCGGCTCCCAAGTGTGGATTACAGGCAT 126
DB      242 CTCTGACCTCGTATCGCCGCGCTCGGCTCCCAAGTGTGGATTACAGGCAT 186

```

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Search completed: May 24, 2004, 18:20:09
Job time : 73 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2004, 14:16:21 ; Search time 71 Seconds
(without alignment)

6776.654 Million cell updates/sec

Title: US-10-621-363-12

Sequence: 1 ccgagttctttctttctt...accaatctcgtgccgaatc B67

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scrolling mode: IDENT11_NVC
Gapop 10.0 , Gapext 1.0
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Searched: 682709 seqs, 27747546 residues

Total number of hits satisfying chosen parameters: 1365418

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database

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1: Issue_Parents NA.*
2: /cgm2_6/prodata/2/ina/5A.COMB.seq.*
3: /cgm2_6/prodata/2/ina/5B.COMB.seq.*
4: /cgm2_6/prodata/2/ina/6A.COMB.seq.*
5: /cgm2_6/prodata/2/ina/6B.COMB.seq.*
6: /cgm2_6/prodata/2/ina/PCBUS.COMB.seq.*
7: /cgm2_6/prodata/2/ina/backfile1.seq.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	130.4	15.0	23255	4	US-09-616-289-51	Sequence 51, Appl
2	124.6	14.4	48312	4	US-09-671-317-485	Sequence 485, Appl
3	124.6	14.4	63000	4	US-09-789-172-18	Sequence 18, Appl
4	124.2	14.3	168575	4	US-09-426-280-1	Sequence 1, Appl
5	123.8	14.3	1712	3	US-09-058-389A-12	Sequence 12, Appl
6	123.8	14.3	1712	4	US-09-611-791-12	Sequence 12, Appl
7	123.8	14.3	6354	3	US-09-058-389A-5	Sequence 5, Appl
8	123.6	14.3	6354	4	US-09-611-791-5	Sequence 5, Appl
9	123.6	14.3	15063	4	US-09-801-052-3	Sequence 3, Appl
10	123.6	14.3	10663	4	US-10-020-121-3	Sequence 3, Appl
11	123	14.2	4922	2	US-08-330-272-5	Sequence 5, Appl
12	123	14.2	4922	5	PCT-US95-1363-5	Sequence 5, Appl
13	123	14.2	128779	4	US-09-497-855A-38	Sequence 38, Appl
14	122.4	14.1	174493	4	US-09-804-471A-3	Sequence 3, Appl
15	122.4	14.1	174493	4	US-10-238-709-3	Sequence 3, Appl
16	122	14.1	155331	3	US-09-128-155-16	Sequence 16, Appl
17	122	14.1	175373	3	US-09-128-155-17	Sequence 17, Appl
18	121.8	14.0	43950	4	US-09-735-934A-3	Sequence 3, Appl
19	121.8	14.0	43950	4	US-10-060-332-3	Sequence 3, Appl
20	121.8	14.0	148567	4	US-09-801-876B-3	Sequence 3, Appl
21	121.8	14.0	148567	4	US-10-254-869-3	Sequence 3, Appl
22	121.6	14.0	429	4	US-09-621-976-9533	Sequence 9533, Appl
23	121.6	14.0	534	1	US-08-599-252-101	Sequence 101, Appl
24	121.6	14.0	534	5	PCT-US96-06552-101	Sequence 101, Appl
25	121.6	14.0	534	5	PCT-US96-06583-101	Sequence 101, Appl
26	121.2	14.0	8224	2	US-09-010-358-14	Sequence 14, Appl
27	121.2	14.0	8224	3	US-09-366-260-14	Sequence 14, Appl

C	28	1.21	14.0	521	4	US-09-621-976-11392	Sequence 11392, A
	29	121	14.0	1744	4	US-09-511-625B-19	Sequence 19, App
	30	121	14.0	17425	4	US-09-511-605B-31	Sequence 5, Appl
	31	120.8	13.9	2280	4	US-09-702-707-351	Sequence 321, App
	32	120.8	13.9	2280	4	US-09-736-467-321	Sequence 321, App
	33	120.8	13.9	2280	4	US-09-614-124B-21	Sequence 321, App
	34	120.8	13.9	2280	4	US-09-617-328-321	Sequence 321, App
	35	120.8	13.9	2280	4	US-09-589-168-321	Sequence 46, App
	36	120.8	13.9	41100	4	US-09-755-665-46	Sequence 10, Appl
	37	120.6	13.9	7210	2	US-08-257-963B-10	Sequence 10, Appl
	38	120.6	13.9	7210	4	US-08-367-841A-10	Sequence 10, Appl
	39	120.6	13.9	7210	5	US-08-520-373D-4	Sequence 10, Appl
	40	120.6	13.9	14581	4	US-08-520-373D-4	Sequence 43, Appl
	41	120.6	13.9	22481	4	US-08-367-841A-3	Sequence 43, Appl
	42	120.6	13.9	22481	5	US-08-367-841A-3	Sequence 43, Appl
	43	120.6	13.9	22484	4	US-09-875-223-2	Sequence 2, Appl
	44	120.6	13.9	22484	4	US-09-875-223-2	Sequence 2, Appl
	45	120.6	13.9	66804	4	US-09-740-041-3	Sequence 3, Appl

ALIGNMENTS

```

RESULT 1
US-09-616-289--51
Sequence 51, Application US/09616289
Patent No. 6632823
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT FILING DATE: US/09/616, 289
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/511,849
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 51
LENGTH: 22255
TYPE: DNA
ORGANISM: Homo sapiens
US-09-616-289-51

Query Match      15.0%; Score 130.4; DB 4; Length 22255;
Best Local Similarity 89.7%; Pred. No. 8.1e-30;
Matches 140; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY      6   TTTT TTTT TTTT TTTT TTAAGTAGGATGGCGCTTCACCGCTGTAGCCAGATGCGT    65
DB      7346  TTTTTTTTTTTTTTTTTTTTATTAGTAGACACGGGGTTTCAACCGTGTTAGCCAGATGCGT    74005

QY      66   CGAAGCTCCTGACCTCGATCGGCCCGCGCTCGGCCTCCCAAAGTCTGGGATTACAGGCA    125
DB      7406   CGATCTGTAACTCGATCGGCCCGCGCTCGGCCTCCCAAAGTCTGGGATTACAGGCT    74685

QY      126  TGAGCCACTGGCCCCACCGCGCTCTTTTAAACATTC    161
DB      7466  TGAGCCACACAGCGCTGGCCTATTATTATTATTATTC    7501

```

```
Sequence 485, Application US/09671317
Patent No. 6528260
GENERAL INFORMATION:
APPLICANT: Blumentfeld, Marta
APPLICANT: Chumakov, Ilya
APPLICANT: Bouguetere, Lydie
TITLE OF INVENTION: BIALLELIC MARKERS RELATED TO GENES INVOLVED IN DRUG METABOLISM
FILE REFERENCE: 62-US3.CIF
CURRENT APPLICATION NUMBER: US/09/671,117
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 09/536,178
PRIOR FILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: PCT/IB00/00403
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/126,269
PRIOR FILING DATE: 1999-03-25
PRIOR APPLICATION NUMBER: US 60/131,961
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 977
SOFTWARE: Patent.pm
SEQ ID NO 485
LENGTH: 49312
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 5466..7466
OTHER INFORMATION: 5' regulatory region
NAME/KEY: exon
LOCATION: 7467..7725
OTHER INFORMATION: exon 1
NAME/KEY: exon
LOCATION: 70256..20355
OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 36905..36975
OTHER INFORMATION: exon 3
NAME/KEY: exon
LOCATION: 45167..45248
OTHER INFORMATION: exon 4
NAME/KEY: exon
LOCATION: 45728..45965
OTHER INFORMATION: exon 5
NAME/KEY: misc_feature
LOCATION: 45966..49312
OTHER INFORMATION: 3' regulatory region
NAME/KEY: allele
LOCATION: 7654
OTHER INFORMATION: 10-286-289 : polymorphic base G or C
NAME/KEY: allele
LOCATION: 7619
OTHER INFORMATION: 10-286-345 : polymorphic base A or T
NAME/KEY: allele
LOCATION: 7649
OTHER INFORMATION: 10-286-375 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 17258
OTHER INFORMATION: 12-425-57 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 21590
OTHER INFORMATION: 12-421-135 : insertion of T
NAME/KEY: allele
LOCATION: 21595
OTHER INFORMATION: 12-421-140 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 36971
OTHER INFORMATION: 10-523-232 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 45214
OTHER INFORMATION: 10-289-201 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 45741
OTHER INFORMATION: 10-290-37 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 46029
OTHER INFORMATION: 10-290-326 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 46032
OTHER INFORMATION: 10-290-328 : deletion of G
NAME/KEY: primer_bind
LOCATION: 7276..7294
OTHER INFORMATION: 10-286.pu
NAME/KEY: primer_bind
LOCATION: 7676..7694
OTHER INFORMATION: 10-286.rp complement
NAME/KEY: primer_bind
LOCATION: 16839..16856
OTHER INFORMATION: 12-425.rp
NAME/KEY: primer_bind
LOCATION: 17297..17314
OTHER INFORMATION: 12-425.pu complement
NAME/KEY: primer_bind
LOCATION: 21456..21474
OTHER INFORMATION: 12-421.pu
NAME/KEY: primer_bind
LOCATION: 21886..21906
OTHER INFORMATION: 12-421.rp complement
NAME/KEY: primer_bind
LOCATION: 36740..36758
OTHER INFORMATION: 10-523.pu
NAME/KEY: primer_bind
LOCATION: 36997..37015
OTHER INFORMATION: 10-523.rp complement
NAME/KEY: primer_bind
LOCATION: 45020..45037
OTHER INFORMATION: 10-289.pu
NAME/KEY: primer_bind
LOCATION: 45413..45432
OTHER INFORMATION: 10-289.rp complement
NAME/KEY: primer_bind
LOCATION: 45705..45724
OTHER INFORMATION: 10-290.pu
NAME/KEY: primer_bind
LOCATION: 46104..46123
OTHER INFORMATION: 10-290.rp complement
NAME/KEY: primer_bind
LOCATION: 7545..7563
OTHER INFORMATION: 10-286-289.mis
NAME/KEY: primer_bind
LOCATION: 7565..7583
OTHER INFORMATION: 10-286-289.mis complement
NAME/KEY: primer_bind
LOCATION: 7600..7618
OTHER INFORMATION: 10-286-345.mis
NAME/KEY: primer_bind
LOCATION: 7620..7638
OTHER INFORMATION: 10-286-345.mis complement
NAME/KEY: primer_bind
LOCATION: 7630..7648
OTHER INFORMATION: 10-286-375.mis
NAME/KEY: primer_bind
LOCATION: 7650..7668
OTHER INFORMATION: 10-286-375.mis complement
NAME/KEY: primer_bind
LOCATION: 17239..17257
OTHER INFORMATION: 12-425-57.mis
NAME/KEY: primer_bind
LOCATION: 17259..17277
OTHER INFORMATION: 12-425-57.mis complement
NAME/KEY: primer_bind
LOCATION: 21576..21594
OTHER INFORMATION: 12-421-140.mis
NAME/KEY: primer_bind
LOCATION: 21596..21614
OTHER INFORMATION: 12-421-140.mis complement
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NAME/KEY: primer_bind
LOCATION: 36952..36970
OTHER INFORMATION: 10-523-232.mis
NAME/KEY: primer_bind
LOCATION: 36972..36990
OTHER INFORMATION: 10-523-232.mis complement
NAME/KEY: primer_bind
LOCATION: 45195..45213
OTHER INFORMATION: 10-289-201.mis
NAME/KEY: primer_bind
LOCATION: 45215..45233
OTHER INFORMATION: 10-289-201.mis complement
NAME/KEY: primer_bind
LOCATION: 45722..45740
OTHER INFORMATION: 10-290-37.mis
NAME/KEY: primer_bind
LOCATION: 45742..45760
OTHER INFORMATION: 10-290-37.mis complement
NAME/KEY: primer_bind
LOCATION: 46010..46028
OTHER INFORMATION: 10-290-326.mis
NAME/KEY: primer_bind
LOCATION: 46030..46048
OTHER INFORMATION: 10-290-326.mis complement
NAME/KEY: misc_binding
LOCATION: 7552..7576
OTHER INFORMATION: 10-286-289.probe
NAME/KEY: misc_binding
LOCATION: 7607..7631
OTHER INFORMATION: 10-286-345.probe
NAME/KEY: misc_binding
LOCATION: 7637..7661
OTHER INFORMATION: 10-286-375.probe
NAME/KEY: misc_binding
LOCATION: 17246..17270
OTHER INFORMATION: 12-425-57.probe
NAME/KEY: misc_binding
LOCATION: 21583..21607
OTHER INFORMATION: 10-523-232.probe
NAME/KEY: misc_binding
LOCATION: 36953..36983
OTHER INFORMATION: 10-289-201.probe
NAME/KEY: misc_binding
LOCATION: 45202..45226
OTHER INFORMATION: 10-289-201.probe
NAME/KEY: misc_binding
LOCATION: 45725..45753
OTHER INFORMATION: 10-290-37.probe
NAME/KEY: misc_binding
LOCATION: 46017..46041
OTHER INFORMATION: 10-290-326.probe
US-09-671-317-485
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Query Match 14.4% Score 124.6; DB 4; Length 49312;
Best Local Similarity 90.5%; Pred. No. 7.9e-28;
Matches 133; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 11 TTTTATTTTAAAGTAGAGATGGGTTTCAACGCTGTAGCCAGATGTTCTGAC 70
DB 33574 TTTTATTTTAAAGTAGAGATGGGTTTCAACGCTGTAGCCAGATGTTCTGAC 33633

QY 71 TCTGACCTGCTATTCGCGCCCTCGGCTCCCAAGTGTGGATTACAGGATAGC 130
DB 33634 TCTGACCTGCTATTCGCGCCCTCGGCTCCCAAGTGTGGATTACAGGATAGC 33693

QY 131 CACTGCGCCAGCGGCTCTTTTAAAC 157
DB 33694 CACTGCGCCAGCGGATTTTCAATC 33720

RESULT 3
US-09-780-172-18/c
; Sequence 18, Application US/09780172
```

```
Patent No. 6607916
GENERAL INFORMATION:
APPLICANT: Robert McKay
APPLICANT: Susan M. Freiler
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-ALPHA EXPRESSION
FILE REFERENCE: RFS-0159
CURRENT APPLICATION NUMBER: US/09/780,172
NUMBER OF SEQ ID NOS: 96
SEQ ID NO 18
LENGTH: 63000
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
US-09-780-172-18
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Query Match 14.4% Score 124.6; DB 4; Length 63000;
Best Local Similarity 90.5%; Pred. No. 9e-28;
Matches 133; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
```

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QY 6 TTTTATTTTAAAGTAGAGATGGGTTTCAACGCTGTAGCCAGATGTTCT 65
DB 26204 TTTTATTTTAAAGTAGAGATGGGTTTCAACGCTGTAGCCAGATGTTCT 26145

QY 66 CGAATCTGACCTGTGATCCGCCCTCGGCTCCCAAGTGTGGATTACAGCA 125
DB 26144 CGATCTCGACCTGTGATCCGCCCTCGGCTCCCAAGTGTGGATTACAGCA 26085

QY 126 TGAGCCACTGCGCCAGCGGCTTTT 152
DB 26084 TGAGCCACTGCGCCAGCGGCTTTT 26058
```

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RESULT 4
US-09-426-290-1/c
; Sequence 1, Application US/09426290
; Patent No. 6410712
GENERAL INFORMATION:
APPLICANT: Berglind Ran Olafsdottir
APPLICANT: Jeffrey Gulcher
TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
FILE REFERENCE: 2345 2001-000
CURRENT APPLICATION NUMBER: US/09/426,290
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 168575
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
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NAME/KEY: CDS
LOCATION: (21181)...(21403)
NAME/KEY: CDS
LOCATION: (95252)...(95430)
NAME/KEY: CDS
LOCATION: (101753)...(101996)
NAME/KEY: CDS
LOCATION: (110324)...(110439)
NAME/KEY: CDS
LOCATION: (124058)...(124278)
NAME/KEY: CDS
LOCATION: (127009)...(127130)
NAME/KEY: CDS
LOCATION: (128910)...(129139)
US-09-426-290-1
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Query Match 14.3% Score 124.2; DB 4; Length 168575;
Best Local Similarity 83.4%; Pred. No. 2.1e-27;
Matches 141; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
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QY 7 TTTTATTTTAAAGTAGAGATGGGTTTCAACGCTGTAGCCAGATGTTCTC 66
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Fri May 28 12:50:58 2004

us-10-621-363-12_1.rn1

Page 4

Db 71067 TTTTGTGATTTTGTGAGATGGGGTTTACCGTGTAGCCAGAGATGCTGTG 71008
67 GAGCTCTGACCTGATGATCCGCGCTCCGCTCCCAAGTCTGGGATTACAGCAT 126
Db 71007 GATCTCCGATCTGTGATCTGACCGCTCCGCTCCCAAGTCTGGGATTACAGCAT 70948
Cy 127 GAGCAGCTGCGCCGCGCTCTTTTAACTATCCCGAGACTGTACA 175
Db 70947 GAGCAGCTGCGCCGCGCTCTTTTAACTATCCCGAGACTGTACA 70899

RESULT 5
US-09-058-389A-12
Sequence 12, Application US/09058389A
Patent No. 6130065

GENERAL INFORMATION:
APPLICANT: Belt, Judith A.
APPLICANT: Crawford, Charles R.
APPLICANT: Patel, Divyen
TITLE OF INVENTION: A NITROBENZYLAMERCAPOURINERIBOSIDE
TITLE OF INVENTION: (NEMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSPORT
TITLE OF INVENTION: PROTEIN, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
TITLE OF INVENTION: USE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSES: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,389A
FILING DATE: April 9, 1998
CLASSIFICATION: 800
TELECOMMUNICATION INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-013N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-343-1684
TELEFAX: 201-487-5800

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1712 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "intron 2"
HYPOTHETICAL: NO
US-09-058-389A-12

Query Match 14.3%; Score 123.8; DB 3; Length 1712;
Best Local Similarity 81.7%; Pred. No. 2.3e-28;
Matches 143; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Db 526 CGCGGCTATTTTGTGATTTTGTAGTGAAGAGCGGGTTTACCGTGTAGCCAGATG 585
Cy 62 GTCTGGAATCTGACCTGATGATCCGCGCTGCGCTCCCAAGTCTGGGATTACA 121
Db 586 GTCTGGAATCTGACCTGATGATCCGCGCTGCGCTCCCAAGTCTGGGATTACA 645
Cy 122 GGATGAGCACTGCGCCAGCGCTCTTTTAACTATCCCGAGACTGTACA 176

Db 646 GGCGTACGACCGTCCGCGCTCTTCACTCAACAACTTTAGTGTCACTACTG 700

RESULT 6
US-09-611-781-12
Sequence 12, Application US/09611781
Patent No. 6423829

GENERAL INFORMATION:
APPLICANT: Belt, Judith A.
APPLICANT: Crawford, Charles R.
APPLICANT: Patel, Divyen
TITLE OF INVENTION: A NITROBENZYLAMERCAPOURINERIBOSIDE
TITLE OF INVENTION: (NEMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSPORT
TITLE OF INVENTION: PROTEIN, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
TITLE OF INVENTION: USE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSES: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/611,781
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/058,389
FILING DATE: April 9, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-013N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-343-1684
TELEFAX: 201-487-5800

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1712 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "intron 2"
HYPOTHETICAL: NO
US-09-611-781-12

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Best Local Similarity 81.7%; Pred. No. 2.3e-28;
Matches 143; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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Cy 62 GTCTGGAATCTGACCTGATGATCCGCGCTGCGCTCCCAAGTCTGGGATTACA 121
Db 586 GTCTGGAATCTGACCTGATGATCCGCGCTGCGCTCCCAAGTCTGGGATTACA 645
Cy 122 GGATGAGCACTGCGCCAGCGCTCTTTTAACTATCCCGAGACTGTACA 176
Db 646 GGCGTACGACCGTCCGCGCTCTTCACTCAACAACTTTAGTGTCACTACTG 700

RESULT 7

Fri May 28 12:50:58 2004

us-10-621-363-12_1.rnt

Page 5

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US-09-058-389A-5
; Sequence 5, Application US/09058389A
; Patent No. 613065
; GENERAL INFORMATION:
; APPLICANT: Belt, Judith A.
; APPLICANT: Crawford, Charles R.
; APPLICANT: Patel, Divyen
; TITLE OF INVENTION: A NITROBENZYL MERCAPTOPURINE RIBOSIDE
; TITLE OF INVENTION: (NMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSPORT
; TITLE OF INVENTION: PROTEIN, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
; TITLE OF INVENTION: USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESS: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/058,389A
; FILING DATE: April 9, 1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-013N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6354 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; US-09-058-389A-5

Query Match      14.3%; Score 123.8; DB 3; Length 6354;
Best Local Similarity 81.7%; Pred. No. 4.6e-28;
Matches 143; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 2 CGAGTTTATTTTATTTTATTTTAAAGTAGAGATGCGGTTTACCGGTGTTAGCCAGGANG 61
DB 1111 CGCGGCTATTTTATTTTATTTTATTTAGTAGAGACGGGTTTACCGGTGTTAGCCAGGANG 1170
QY 62 GTCTGCACTCTGACCTGATTCGCGCGCTCGCGCTCCCAAGTGTGGATTACA 121
DB 1171 GTCTGCACTCTGACCTGATTCGCGCGCTCGCGCTCCCAAGTGTGGATTACA 1230
QY 122 GCGATGACCACTGCGCCGACCGCGGTCCTTTTAAACATTTCCCGAGCTGTACAG 176
DB 1231 GCGGTGACCACTGCGCCGACCGCGGTCCTTTTAAACATTTAGTGTGATCTACTG 1285

RESULT 8
US-09-611-781-5
; Sequence 5, Application US/09611781
; Patent No. 6423829
; GENERAL INFORMATION:
; APPLICANT: Belt, Judith A.
; APPLICANT: Crawford, Charles R.
; APPLICANT: Patel, Divyen
; TITLE OF INVENTION: A NITROBENZYL MERCAPTOPURINE RIBOSIDE
; TITLE OF INVENTION: (NMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSPORT
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```
; TITLE OF INVENTION: PROTEIN, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
; TITLE OF INVENTION: USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESS: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/611,781
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/058,389
; FILING DATE: April 9, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-013N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6354 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; US-09-611-781-5

Query Match      14.3%; Score 123.8; DB 4; Length 6354;
Best Local Similarity 81.7%; Pred. No. 4.6e-28;
Matches 143; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 2 CGAGTTTATTTTATTTTATTTTAAAGTAGAGATGCGGTTTACCGGTGTTAGCCAGGANG 61
DB 1111 CGCGGCTATTTTATTTTATTTTATTTAGTAGAGACGGGTTTACCGGTGTTAGCCAGGANG 1170
QY 62 GTCTGCACTCTGACCTGATTCGCGCGCTCGCGCTCCCAAGTGTGGATTACA 121
DB 1171 GTCTGCACTCTGACCTGATTCGCGCGCTCGCGCTCCCAAGTGTGGATTACA 1230
QY 122 GCGATGACCACTGCGCCGACCGCGGTCCTTTTAAACATTTCCCGAGCTGTACAG 176
DB 1231 GCGGTGACCACTGCGCCGACCGCGGTCCTTTTAAACATTTAGTGTGATCTACTG 1285

RESULT 9
US-09-801-052-3/C
; Sequence 3, Application US/09801052
; Patent No. 6368842
; GENERAL INFORMATION:
; APPLICANT: BEASLEY, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: C1001045
; CURRENT APPLICATION NUMBER: US/09/801,052
; CURRENT FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 16063
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1 NAME: Mistrock, S. Leslie
2 REGISTRATION NUMBER: 18,872
3 REFERENCE/DOCKEN NUMBER: 6754-027
4 TELECOMMUNICATION INFORMATION:
5
6 TELEPHONE: (212) 790-0900
7
8 TELEFAX: (212) 790-8864/9741
9
10 TELEX: 66141 PENNIE
11
12 INFORMATION FOR SEQ ID NO: 5:
13
14 SEQUENCE CHARACTERISTICS:
15
16 LENGTH: 4922 base pairs
17
18 TYPE: nucleic acid
19
20 STRANDEDNESS: unknown
21
22 TOPOLOGY: unknown
23
24 MOLECULE TYPE: DNA
25
26 CDT-US95-13663-5

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Query Match	14.2%	Score 123;	DB 5;	Length 4922;
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			Gaps	0;

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Db	3351	CGAATCCTGACCTCTATATCTGCGCGCTCTGCGCTCCCAAAGTCTGGGATTTAAGGCA	3410
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Db	3411	TGAGCCACCAAGTCTCGGCGCTTATACCATCTTTATT	3445

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RESULT 13
US-09-497-855A-38/c
; Sequence 38, Application US/09497855A
; Patent No. 6605432
;
; GENERAL INFORMATION:
;
; APPLICANT: Huang, Tim
;
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
;
; FILE REFERENCE: UMO1523
;
; CURRENT APPLICATION NUMBER: US/09/497,855A
;
; CURRENT FILING DATE: 2000-02-04
;
; PRIOR APPLICATION NUMBER: 60/120,592
;
; PRIOR FILING DATE: 1998-02-18
;
; PRIOR APPLICATION NUMBER: 60/118,760
;
; PRIOR FILING DATE: 1999-02-05
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; NUMBER OF SEQ ID NOS: 54
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; SOFTWARE: Patentin version 3.0
;
; SEQ ID NO 38
;
; LENGTH: 128779
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; TYPE: DNA
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; ORGANISM: Homo sapiens;
;
; US-09-497-855A-38

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Query Match	14.2%	Score 123	DB 4	Length 128779
Best Local Similarity	92.8%	Pred. No. 4.2e-27		
Matches 129	Conservative	0	Mismatches 10	Indels 0
				Gaps 0

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Db	17374	CGATCTCTGACCTCGTGATCTCGGCCGACCTCGGCTCTCCAAATGCTGGGATTTACAGGCG	17315
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US-09-804-471A-3/C
; Sequence 3, Application US/09804471A
; Patent No. 6479269
; GENERAL INFORMATION
; APPLICANT: WEBSTER, Marion et al
; TITLE OP INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OP INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OP INVENTION: THEREOF
; FILE REFERENCE: C0001164
; CURRENT APPLICATION NUMBER: US/09/804,471A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 174493
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) -- (174493)
; OTHER INFORMATION: n = A,T,C OR G
US-09-804-471A-3

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Query Match	14.14%	Score 122.44	DB 4	Length 174493
Best Local Similarity	89.24%	Pred. No. 7.6e-27		
Matches 132	Conservative 0	Mismatches 16	Indels 0	Gaps 0

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QY	66	CGAATCTCCGAACTCGTGTATCCGCGCGCTCGCCCAAGTGTGGGATTAACAGCA	125
Db	88941	CGATCTCCAGCTCTAGATCTGCGCGCTCGACCTCCAAATGTCTGGGATTAACAGCG	88882
QY	126	TGAGCCACTGCGCCGACCGGCTTTT	153
Db	88881	TGAGCCACTGCGCCGACCGCTTTTCTT	88854

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RESULT 15
US-10-238-709-3/c
: Sequence 3, Application US/10238709
: Patent No. 6680188
: GENERAL INFORMATION:
: APPLICANT: WEBSTER, Marion et al
: TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
: TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
: TITLE OF INVENTION: THEREOF
: FILE REFERENCE: C0001164DIV
: CURRENT APPLICATION NUMBER: US/10/238, 709
: CURRENT FILING DATE: 2002-09-11
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: Fasteq For Windows Version 4.0
: SEQ ID NO 3
: LENGTH: 174493
: TYPE: DNA
: ORGANISM: Human
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (1)...(174493)
: OTHER INFORMATION: n = A,T,C or G
US-10-238-709-3

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Query March	14.1%	Score 122.4	DB 4	Length 174493
Best Local Similarity	89.2%	Pred. No. 7.6e-27		
Matches 132, Conservative	0	Mismatches 16	Indels 0	Gaps 0

QY	6	T T T T T T T T T T T T T T A G T G A G A T G G G T T T A C C G T G A G C A G A G T C T	65
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Db	88941	CGATCTCCTGACCTCATGATCTGCCCGCTCAGCCTCCCAAGTGTGGATTACAGGAG	88882
Qy	126	TGAGCCACTGCGGCCAGCGCGTCTTTT	153
Db	88881	TGAGCCACTGCGGCCAGCGCGTCTTTTCTT	88854

Search completed: May 24, 2004, 15:50:37
 Job time : 74 secs

Fri May 28 12:50:58 2004

us-10-621-363-12_1.rst

Page 2

Pax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 26 Row: b Column: 04
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1. 586
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/clone_lib="Human Retinal Pigment epithelium/choroid cDNA
(Un-normalized, unamplified): cs"
/note="Organ: Eye; Vector: pCMVSPORT6; Two different donor
eyes (75-80 years old) yielded approximately 600 mg of
dissected RPE/choroid tissue. This in turn yielded 340 ug
of total RNA and 7 ug of mRNA. A directionally cloned cDNA
library in the pCMVSPORT6 vector was constructed at Life
Technologies (Rockville, MD; now part of Invitrogen Corp),
essentially following the protocols of the Superscript
Plasmid System (Invitrogen Corp).
<http://www.invitrogen.com/>: The library code
designation was cs. For this library, cDNA inserts were
cloned into the NotI/MluI sites of the vector. EST
analysis was performed on the unamplified library at the
NIH Intramural Sequencing Center (NISC)."

ORIGIN

Query Match 64.6%; Score 560; DB 14; Length 586;
Best Local Similarity 99.3%; Pred. No. 4e-96;
Matches 582; Conservative 1; Mismatches 1; Indels 2; Gaps 2;
27 AGTAGAGATGGGTTTACCGGTGAGCCAGAGAGTCTGGAACCTCTGACCTGGATC 86
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526 CGCCCGCTCGGCTCCCAAGTCTGGGATTACAGGAGTACGACCTGCGCCACCGG 467
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466 TCTTTTAAACATTCCTCCAGAGTCTGACGACCAACCACTCACTGACCTGATTTGGGAC 407
207 TCCCGCCAGCGGCACTGATCTGACAGAGTGAAGCAAGCAAGCAAGTGGGGATTC 266
406 TCCCGCCAGCGGCACTGATCTGACAGAGTGAAGCAAGCAAGCAAGTGGGGATTC 347
267 ACATCTAAGGCTGTGATGAGTGAAGAGAGAGATCAAGCAAGCAAGCAAGTGGG 326
346 ACATCTAAGGCTGTGATGAGTGAAGAGAGAGATCAAGCAAGCAAGCAAGTGGG 287
327 GCTTTTCTTACCAACACCTCTCTGCTCCCACTGCTTTTGAAGGGGCAAGATATG 386
286 GCTTTTCTTACCAACACCTCTCTGCTCCCACTGCTTTTGAAGGGGCAAGATATG 227
387 GGGCA-GCTGCCCACTGCTACAGTGAAGAGAGATGAGAAATCTGACCTTTGAGGTG 445
226 GGGCAAGGCTGCCCACTGCTACAGTGAAGAGAGATGAGAAATCTGACCTTTGAGGTG 167
446 CTCGCCCTCTTACAGCAGCTCTTAAAGCAATGACCCCAAGGGAG-CTTACACA 504
166 CTCGCCCTCTTACAGCAGCTCTTAAAGCAATGACCCCAAGGGAGCTTACACA 107
505 AGTTCACAAGGCGGCAATGATTCATGAGAGAGGGGAGAGGCAAGAGACTCCGGAGAGA 564
106 AGTTCACAAGGCGGCAATGATTCATGAGAGAGGGGAGAGGCAAGAGACTCCGGAGAGA 47
565 GAGGCCCAATAGGCTGTGCTATTTCCATCCATCAGAGAGGAG 610
46 GAGGCCCAATAGGCTGTGCTATTTCCATCCATCAGAGAGGAG 1

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VERSION CA392562.1 GI:24725401
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 586)
Mistow, G., Bernstein, S.L., Wyatt, M.K., Parris, R.N., Behal, A.,
Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.
Expressed sequence tag analysis of human RPE/choroid for the
NIH Bank Project: Over 6000 non-redundant transcripts, novel genes
and splice variants
Mol. Vis. 8 (4), 205-220 (2002)
22103460
12107410

JOURNAL MEDLINE
PUBMED
COMMENT Contact: Mistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 26 Row: b Column: 05
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1. 586
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/clone_lib="Human Retinal pigment epithelium/choroid cDNA
(Un-normalized, unamplified): cs"
/note="Organ: Eye; Vector: pCMVSPORT6; Two different donor
eyes (75-80 years old) yielded approximately 600 mg of
dissected RPE/choroid tissue. This in turn yielded 340 ug
of total RNA and 7 ug of mRNA. A directionally cloned cDNA
library in the pCMVSPORT6 vector was constructed at Life
Technologies (Rockville, MD; now part of Invitrogen Corp),
essentially following the protocols of the Superscript
Plasmid System (Invitrogen Corp).
<http://www.invitrogen.com/>: The library code
designation was cs. For this library, cDNA inserts were
cloned into the NotI/MluI sites of the vector. EST
analysis was performed on the unamplified library at the
NIH Intramural Sequencing Center (NISC)."

FEATURES

Query Match 64.6%; Score 560; DB 14; Length 586;
Best Local Similarity 99.3%; Pred. No. 4e-96;
Matches 582; Conservative 1; Mismatches 1; Indels 2; Gaps 2;
27 AGTAGAGATGGGTTTACCGGTGAGCCAGAGAGTCTGGAACCTCTGACCTGGATC 86
586 AGTAGAGATGGGTTTACCGGTGAGCCAGAGAGTCTGGAACCTCTGACCTGGATC 527
87 CGCCCGCTCGGCTCCCAAGTCTGGGATTACAGGAGTACGACCTGCGCCACCGG 146
526 CGCCCGCTCGGCTCCCAAGTCTGGGATTACAGGAGTACGACCTGCGCCACCGG 467
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Dd		346	ACATTTAAGTCTGGTGAATGGCTGTAGTAAGAAGAGAAAGATCAGGAAACAAAGCCTTAG	287
Oy		327	GTCCTTTCTTACACAAACACCTCTCTGCCACCTGCTTTGAAAGGGGACAGAGTATAGTG	386
Dd		286	GTCCTTTCTTACACAAACACCTCTCTGCCACCTGCTTTGAAAGGGGACAGAGTATAGTG	227
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Dd		166	CTGGCCCTCTTCATCAGCCAGCTCTAACCTTAAGCCAATGATGCCCAAGGAGCCTTACACA	107
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LOCUS				
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VERSION				
KEYWORDS				
SOURCE				
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
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mRNA sequence.				
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AUTHORS				
Melton,D., Brown,J., Kenty,G., Penmutt,A., Lee,C., Kaestner,K.,				
Lemishka,I., Scearca,M., Brestelli,J., Gradwohl,G., Clifton,S.,				
Hillier,L., Maria,M., Page,D., Wylie,T., Martin,J., Blisstein,A.,				
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,				
Cardenas,M., Gibbons,M., McComar,R., Cole,R., Teagareishvili,R.,				
Williams,T., Jackson,Y. and Bowers,Y.				
Endocrine Pancreas Consortium				
Unpublished (2000)				
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue				

Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dme1@mcdbiochem.harvard.edu
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
 Washington University Genome Sequencing Center For information on
 obtaining a clone please contact: Dr. Hiroshi Inoue
 (hinoue@im.wustl.edu)
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 High quality sequence stop: 450.
 Location/Qualifiers
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/clone lib="HR85.islet"
/robe="Organ: Pancreas; Vector: pBluescript SK(-); Site_1
Nuclei_Site_2: XhoI; CDNA made by oligo-dT priming
Size-selected on agarose gel. Average insert size ~1kb. 5
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hironshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoe@ingate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2632."

```

Query Match	58.0%;	Score 502.6;	DB 14;	Length 527;
Best Local Similarity	99.44%;	Pred. No. 3e-85;	Mismatches 0;	Gaps 2;
Matches 524;	Conservative 1;			
QY	22	TTTTAAGTAGAGATGAGGAGTTTACCGGTGTTAGCCAGGATGCTCTCGAACTCTCTGACCTCG	81	
Db	1	TTTTAAGTAGAGATGAGGAGTTTACCGGTGTTAGCCAGGATGCTCTCGAACTCTCTGACCTCG	60	
QY	82	TGATTCGCGCGCCCTCGCGCTCCGCAAAAGTGTGGGATTAACAGGCAATGAGCCACTCGGCCCA	141	
Db	61	TGATTCGCGCGCCCTCGCGCTCCGCAAAAGTGTGGGATTAACAGGCAATGAGCCACTCGGCCCA	120	
QY	142	GCCGGTCTTTTAAACATTCCCGAGACGTGTACAGCCAAACCATACTCACTGCATTTTG	201	
Db	121	GCCGGTCTTTTAAACATTCCCGAGACGTGTACAGCCAAACCATACTCACTGCATTTTG	180	
QY	202	GGAACTCCCCCCCCCAGCGCATPACTGTATCTGTCAGAGGTTAGACCAAGAGCAAGATPAGGG	261	
Db	181	GGAACTCCCCCCCCCAGCGCATPACTGTATCTGTCAGAGGTTAGACCAAGAGCAAGATPAGGG	240	
QY	262	GATTCACACTCTAAGGCTGTGTATGCTGTATGAAGAAAGAAAGAAATCAGCGAACTAAAGCC	321	
Db	241	GATTCACACTCTAAGGCTGTGTATGCTGTATGAAGAAAGAAAGAAATCAGCGAACTAAAGCC	300	
QY	322	TCATAGGCTTCTCTTACCAACAACACTCTGCGCCACCTGTGTTGAAGAGGCGACAAGTA	381	
Db	301	TCATAGGCTTCTCTTACCAACAACACTCTGCGCCACCTGTGTTGAAGAGGCGACAAGTA	360	
QY	382	TATGAGGCGCA-GCTGCCCAACCTGTCTACAGTGAAGGATCTGAGAAATTACTCACTTTG	440	
Db	361	TATGAGGCGAGGCTGCCCAACCTGTCTACAGTGAAGGATCTGAGAAATTACTCACTTTG	420	
QY	441	AGGCGCTCGCCCTCTTCAATACAGCAGCTCTPACTTAAGCCAAATGACCCCAAGGAG-CTT	499	
Db	421	AGGCGCTCGCCCTCTTCAATACAGCAGCTCTPACTTAAGCCAAATGACCCCAAGGAGCTT	480	
QY	500	AACACAGTCCAAACAGGCCCAATGATTCATGAGCAAGGCGGAGGCC	546	
Db	481	AACACAGTCCAAACAGGCCCAATGATTCATGAGCAAGGCGGAGGCC	527	
RESULT 4				
AM193512				
LOCUS				
DEFINITION	AM193512	491 bp	mRNA	linear
ACCESSION	xm17b12.x1	NCI_CGAP	Uc4	Homo sapiens cDNA clone IMAGE:2654447
VERSION				3
KEYWORDS				similar to contains Alu repetitive element; contains element HGR
ORGANISM	AM193512.1	GI:6472211		
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
TITLE				
COMMENT				

Email: cgaabs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNML at: www-bio.llnl.gov/birop/image/image.html
 Seq primer: -300P from G1bco
 High quality sequence stop: 395.
 Location/Qualifiers

FEATURES

source
 1. 491
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:268447"
 /tissue_type="serous papillary carcinoma, high grade, 2 pooled tumors"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP U4"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.48 kb. Life Technologies catalog #: 1542-016"

ORIGIN

Query Match 54.0%; Score 468.4; DB 10; Length 491;
 Best Local Similarity 99.6%; Pred. No. 9.1e-79;
 Matches 489; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

19 TTTTAAAGTAAAGATGGGTTTCAACCGTGTATACCAAGATGCTCTGCACTCTGACC 78
 1 TTTTAAAGTAAAGATGGGTTTCAACCGTGTATACCAAGATGCTCTGCACTCTGACC 60
 79 TCGTGAATCCGCGCCGCTGCGCTCCCAAGATGGCGGATTAACAGCATGAGCACTGCC 138
 61 TCGTGAATCCGCGCCGCTGCGCTCCCAAGATGGCGGATTAACAGCATGAGCACTGCC 120
 139 CCAAGCGGCTTTTAAACATTCGCCAGACTGTACAGCAACCATATCTCACTGACAT 198
 121 CCAAGCGGCTTTTAAACATTCGCCAGACTGTACAGCAACCATATCTCACTGACAT 180
 199 TTGGGAATCCGCGCCGCTGCGCTCCCAAGATGGCGGATTAACAGCATGAGCACTGCC 258
 181 TTGGGAATCCGCGCCGCTGCGCTCCCAAGATGGCGGATTAACAGCATGAGCACTGCC 240
 259 GGGGATTCACATCTAAGTCTGTGTATGCTGTATGAAGAAGAAATACGCAACAAA 318
 241 GGGGATTCACATCTAAGTCTGTGTATGCTGTATGAAGAAGAAATACGCAACAAA 300
 319 GCGCTTAAGTCTTTTAAACAAACCTCTCTGCCACCTCTTTGAAGGGGAGAA 378
 301 GCGCTTAAGTCTTTTAAACAAACCTCTCTGCCACCTCTTTGAAGGGGAGAA 360
 379 GTATAGTGGGCGA-GCTGCCACCTGCTAAGTGAAGGATCTGAAGAAATCTCAACT 437
 361 GTATAGTGGGCGA-GCTGCCACCTGCTAAGTGAAGGATCTGAAGAAATCTCAACT 420
 438 TTGAAGTCTGCGCTCTTTTCAACAGCAAGCTTAACTTAAGCAACCAACCCGAGAGC 497
 421 TTGAAGTCTGCGCTCTTTTCAACAGCAAGCTTAACTTAAGCAACCAACCCGAGAGC 480
 498 TT 499
 481 CT 482

RESULT 5
 BQ710765/c 941 bp mRNA linear EST 16-JUL-2002
 LOCUS BQ710765
 DEFINITION AGENCOURT 8484953 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:630113
 5', mRNA sequence.

ACCESSION BQ710765
 VERSION BQ710765.1 GI:21849664
 EST
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 941)
 REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (ILNML)
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNML at: http://image.llnl.gov
 Plate: L10C2516 row: h column: 10
 High quality sequence stop: 583.
 Location/Qualifiers

FEATURES

source
 1. 941
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:630113"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 113"
 /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 50.3%; Score 435.8; DB 13; Length 941;
 Best Local Similarity 96.0%; Pred. No. 1e-72;
 Matches 454; Conservative 2; Mismatches 16; Indels 1; Gaps 1;

382 TAGTGGGAGAGCTGCGCACTGCTACAGTGAAGGATCTGGAATATCTCACTTGA 441
 713 TGGGGGAGAGCTGCGCCCTTGAATACAGGAAGGATCTGGAATATCTCACTTGA 654
 442 GGTGCTCGGCTTTTATATGCTGCTCACTTAAGCCATGACCCACGGAG-CTTA 500
 653 GGTGCTCGGCTTTTATATGCTGCTCACTTAAGCCATGACCCACGGAGCTTTC 594
 501 CACAAGTCAACAGAGCCCAATGCAATCATGAGCAGGGGAGCCAAAGACTCCGAG 560
 593 CACAAGTCAACAGAGCCCAATGCAATCATGAGCAGGGGAGCCAAAGACTCCGAG 534
 561 GAGAGAGCCCAATGAGCTGTGTATTTCCGATCATAGAGAGAGAGAGTGGAG 620
 533 GAGAGAGCCCAATGAGCTGTGTATTTCCGATCATAGAGAGAGAGAGTGGAG 474
 621 GCGCTTTGATTAAGTATCATTTCTGAATGCAAGCTTCAAAATCGGGTATGCGGGTG 680
 473 GCGCTTTGATTAAGTATCATTTCTGAATGCAAGCTTCAAAATCGGGTATGCGGGTG 414
 681 AGAATGAGCAGACTTAACCTGAGTGTATAGCAAGCTCCAGGGCGGATGCGCAAG 740
 413 AGAATGAGCAGACTTAACCTGAGTGTATAGCAAGCTCCAGGGCGGATGCGCAAG 354
 741 ACGATCCGCAAGAGAGCTGTGAGCAGACTCTGTGTCCCAAGCACTCGGATTTGAACCC 800
 353 ACGATCCGCAAGAGAGCTGTGAGCAGACTCTGTGTCCCAAGCACTCGGATTTGAACCC 294
 801 GCGCTCTCAAGTCACTGTGTAGCTTGANTGAAYCACTGTCTATGACCAAT 853

Db 293 GGGCTCTCAAGAGCTGCTGTGTAGCTTTGAATGAATGACCTGCTATGACCAAT 241

RESULT 6
LOCUS A1521901
DEFINITION A1521901 421 bp mRNA linear EST 13-APR-1999
t180d03.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2138309 3'
similar to contains A19 repetitive element/contains element P1R5
repetitive element; mRNA sequence.

ACCESSION A1521901 GI:4436036
VERSION A1521901
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 421)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgaps-remail.nih.gov
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrip/image/image.html
Insert Length: 718 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 401.
Location/Qualifiers

FEATURES
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1..421
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2138309"
/lab_host="DH10B"
/clone_lib="NCI CGAP Kid11"
/note="Organ: Kidney; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
plasmid DNA from the normalized library NCI CGAP Kid3 was
prepared, and ss circles were made in vitro. Following RHP
hybridization, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneids 1322376-1323911, 1456007-1456775, and
1500552-1502855). Subtraction by Bento Soares and M.
Facina Bonaldi."

ORIGIN
Query Match 47.2%; Score 409; DB 9; Length 421;
Best Local Similarity 99.8%; Pred. No. 1.7e-67; Indels 1; Gaps 1;
Matches 420; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

22 TTTTAAGTAGAGATGGGTTTACCGTTTAGCCAGAGTGTCTGGAATCTTGACTCG 81
1 TTTTAAGTAGAGATGGGTTTACCGTTTAGCCAGAGTGTCTGGAATCTTGACTCG 60
82 TGAATCCCGCCCGCTCGCTCCCAAGTGTGGGATTACAGGCGATGAGCCACTGGCGCCA 141
Db 61 TGAATCCCGCCCGCTCGCTCCCAAGTGTGGGATTACAGGCGATGAGCCACTGGCGCCA 120
Qy 142 GCCGCTTTTAAACATTTCCCGAGACTGTACAGCCCAACCATCTCACTGACATTG 201
Db 121 GCCGCTTTTAAACATTTCCCGAGACTGTACAGCCCAACCATCTCACTGACATTG 180
Qy 202 GGAATCCCCCGCCGCGCATTAATGATCTGCAAGATTAAGCAAGAGCAAGATGGGG 261

Db 181 GGAATCCCCCGCCGCGCATTAATGATCTGCAAGATTAAGCAAGAGCAAGATGGGG 240

Qy 262 GATTACATCTTAAGTGTGGTGTATGCTGATGAAGAGAAATCGACCAACAAAGCC 321
Db 241 GATTACATCTTAAGTGTGGTGTATGCTGATGAAGAGAAATCGACCAACAAAGCC 300
Qy 322 TTAGGCTTTCTTACCAACACCTCTGTGCCACCTGCTTGAAGAGGGGAGAGTA 381
Db 301 TTAGGCTTTCTTACCAACACCTCTGTGCCACCTGCTTGAAGAGGGGAGAGTA 360
Qy 382 TAGTGGGCGA-GCTGCCACCTGTCTACAGTGAAGGATCTGAGAAATCTCACTTTG 440
Db 361 TAGTGGGCGAGGCTGCCACCTGTCTACAGTGAAGGATCTGAGAAATCTCACTTTG 420
Qy 441 A 441
Db 421 A 421

RESULT 7
LOCUS A1493546
DEFINITION A1493546 392 bp mRNA linear EST 30-MAR-1999
t136b01.x1 NCI CGAP Pauli Homo sapiens cDNA clone IMAGE:2120329 3'
similar to contains A19 repetitive element; mRNA sequence.

ACCESSION A1493546
VERSION A1493546
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 392)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgaps-remail.nih.gov
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrip/image/image.html
Insert Length: 882 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 391.
Location/Qualifiers

FEATURES
source
1..392
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2120329"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP Pauli"
/note="Organ: pancreas; Vector: pCMV-Sport6; Site 1: SalI;
Site 2: NotI. Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"

ORIGIN
Query Match 29.2%; Score 253; DB 9; Length 392;
Best Local Similarity 100.0%; Pred. No. 5.6e-38;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

6 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 65
140 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 199
Qy 66 CGAATCTGAGCTGTGATTCGCGCGCTCGCGCTCCCAAGATGTCTGGATTAAGAGCA 125
Db 200 CGAATCTGAGCTGTGATTCGCGCGCTCGCGCTCCCAAGATGTCTGGATTAAGAGCA 259

QY		126	TGAGCACACTGGGCCCGCCAGCGGCTTTTAAACATTCGCCAGACGTGTACAGCAACCCACT	185
Db		260	TGAGCACACTGGGCCCGCCAGCGGCTTTTAAACATTCGCCAGACGTGTACAGCAACCCACT	319
QY		186	ACTCACCTGAACATTGGGAACCTCCCCCGCCACATAA CTGATCTGCAGAGTAAGACC	245
Db		320	ACTCACCTGAACATTGGGAACCTCCCCCGCCACATAA CTGATCTGCAGAGTAAGACC	379
QY		246	AAGAGCAAGAATG	258
Db		380	AAGAGCAAGAATG	392
<hr/>				
RESULT 8				
LOCUS	AQ387243		574 bp	DNA linear GSS 21-MAY-1999
DEFINITION	RPCII1-154N12.TV RPCI-11 Homo sapiens genomic clone RPCI-11-154N12			
ACCESSION	AQ387243			
VERSION	AQ387243.1		GI:4358266	
KEYWORDS	GSS.			
SOURCE	Homo sapiens (human)			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 574) Zhao,S., Adams,M.D., Nierman,W., Malek,U., de Jong,P. and Venler,J.C. Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building Unpublished (1997) Other GSSs: RPCII1-154N12.TV Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel.: 301 838 0200 Fax: 301 838 0208 Email: hbe@tigr.org Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@djlong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/cdb/hungen/bac_end_search/bac_end_search.html Seq primer: T7 Class: BAC ends.			
FEATURES				
Source	Location/Qualifiers			
	1..574			
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	/mol_type="Genomic DNA"			
	/db_xref="GDB:7559075"			
	/db_xref="taxon:9606"			
	/clone="RPCI-11-154N12"			
	/sex="Male"			
	/cell_type="Lymphocytes"			
	/clone_id="RPCI-11"			
	/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCII Human Male BAC Library"			
ORIGIN				
	15.4%; Score 133.5; DB 28; Length 574;			
	Best Local Similarity 93.9%; Pred. No. 1.8e-15;			
	Matches 139; Conservative 0; Mismatches 9; Indels 0; Gaps 0			
QY	TTTTTTTTTTTTTTTTTAAGTAGAGATGGGAGTTTACCGCTGTAGCCAGATGCTCT	65		
Db	TTTTTTTTTTTTTTTTTTTAAAGTAGAGACGGGGTTTACCGCTGTAGCCAGATGCTCT	86		
QY	CGAAGCTCTGACCTCGATACGCGCCGCTCGGCTCCCAAGATGCTGGAGTTAAGCA	125		
Db	CGATCTCTTGACCTCTGTATCGCCGCTCGGCTCCCAAAATCTGGAGTTAACGGCG	146		

QY	126	TGAGCACTGGCCACCGCCTTTT	153
Db	147	TGAGCCACCGGCCACGCCTTTTTT	174
RESULT 9			
BX504260/c		615 bp	mRNA linear EST 04-SEP-2003
LOCUS			
DEFINITION	DKEZP868620133.f1.686 (synonym: hlcc3)	Homo sapiens CDNA clone	
ACCESSION	DKEZP868620133.5,	mRNA sequence.	
KEYWORDS	BX504260		
VERSION	BX504260.1	GI:32030985	
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 615) Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R., Weges,H.W., Weil,B., Amid,C., Oeanger,A., Fob,G., Han,M. and Wiemann,S. EST (Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R., et al.) Unpublished (2003) Contact: MIPS		
TITLE	MIPS		
JOURNAL	OligoLadeter Landstr.1, D-85764 Neuberg, Germany		
COMMENT	This is the 5' sequence of the clone insert This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de, Sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the CDNA sequencing consortium of the German Genome Project. No si sequence available. This clone (DKEZP868620133) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcencentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers		
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source	1..615		
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	/mol_type="RNA"		
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	/clone="DKEZP868620133"		
	/dev_stage="adult"		
	/lab_host="DH10B"		
	/clone_id="686 (synonym: hlcc3)"		
	/note="Vector: pTriplex2; Site_1: SfiI; Site_2: SfiI; CDNA-collection"		
ORIGIN			
Query Match	15.2%; Score 131.4; DB 13; Length 615;		
Best Local Similarity	99.2%; Pred. No. 4.6e-15;		
Matches 132; Conservative	0; Mismatches 1; Indels 0; Gaps 0;		
QY	2	GCACTTTTATTAAGTAGAAGATGGGATTTCACCGGTTRACGAGAATG	61
Db	136	CGATTTTTTTTTTTTTTTTAACTATAAGATGGGATTTCACCGGTTRACGAGAATG	77
QY	62	GTCCTGAACACTGACCTCGTGATCCGCCCGCCTCGGCTCCGAAAGTGTGAGATTACA	121
Db	76	GTCCTGAACACTGACCTCGTGATCCGCCCGCCTCGGCTCCGAAAGTGTGAGATTACA	17
QY	122	GGCATGAGCACT 134	
Db	16	GGCATGAGCACT 4	
RESULT 10			
AO423092/c		590 bp	DNA linear GSS 23-MAR-1999
LOCUS			
DEFINITION	CITBI-EI.2575M23.TR CITBI-EI Homo sapiens genomic clone 2575M23,		
ACCESSION	AO423092		
	genomic survey sequence.		

us-10-621-363-12_1.rst

VERSION	AQ423092.1	GI:4480816
KEYWORDS	GSS.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

REFERENCE	1 (bases 1 to 590)
AUTHORS	Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shizuya H., Simon, M. and

TITLE	Use of BAC End Sequences from CalTech Libraries for Sequence-Read Mapping
JOURNAL	Map Building
COMMENT	Unpublished (1997)
Other_GSSs	CITB1-BL-2575M2.TF

Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbeet@tigr.org
 Clothes are available from Research Genetics {info@resgen.com}. BAC
 end search page:
http://www.tigr.org/tdb/nunngen/bac_end_search/bac_end_search.html
 Seq primer: M3 Reverse
 Class: BAC ends.

FEATURES	Location/Qualifiers
source	1. .590

OPTIC

Query Match	15.0%	Score 129.8;	DB 28;	Length 590;
Best Local Similarity	95.0%	Pred. No. 9.5e-15;		
Matches 134;	Conservative	0;	Mismatches 7;	Indels 0;
			Gaps	0

[illegible][illegible]

REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE
1	(bases 1 to 699) Donald, M. F., Jernom, G. and Soares, M. B.	Normalization and subtraction: two approaches to facilitate gene discovery	Genome Res. 6 (9), 791-806 (1996)	97044477

PUBMED 8889548
COMMENT Contact: McCray, PB
McCray, PB

University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171

Tissue Procurement: Dr. M. J. Welsh, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com) or from Open Biosystems
 (www.openbiosystems.com).
 The following repetitive elements were found in this cDNA
 sequence: 7-137, α LU (matched complement)
 Seq primer: M13 FORWARD
 POLYA=Yes

FEATURES	location/Qualifiers
source	1. .699

ORGANISM="Homo sapiens"
 mol_type="mRNA"
 db_xref="taxon:9606"
 clone="U1-CF-ECl-adw-o-18-0-U"
 tissue_type="Lung"
 cdiv string="Adult and Fetal"
 lab host="DH10B (Life Technologies) (T1 phage resistant)"
 clone="pYgm-U1-CF-ECl"
 note="Ygm: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; U1-CF-ECl is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetus; day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Geneome Research, 6:791-806, 1996. First strand cDNA, 5' end primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR digested pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the poly(A) tail. The sequence tag for this library is 5'-GAGTGGCTTAC-3'
 TAG_R1808=Normal Lung Epithelial Cells Tissue nos 369-373 and 380-383
 TAG_L18-U1-CF-ECl
 TAG_SEQ=AAGTGGCTTAC"

ORIGIN

Query Match	14.9%	Score 129;	DB 13;	Length 699;
Best Local Similarity	96.4%;	Pred. No. 1.3e-14;		
Matches 132;	Conservative	0;	Mismatches 5;	Indels 0;
			Gaps	0

QY	8	TTTTTTTTTTTTTTTTTAAATAGAGAGGGGTTTACACGGGTATGACAGATGGTCTCG	67
Db	1	TTTTTTTTTTTTTTTTTTCAGTAGAGAGGGGTTTACACGGTGTATGACAGATGGTCTCG	60
QY	68	AACTCTTAAGCTCGTGAATCCGCGCCGCGCTCGCGCTCCCAAGTGTGGGATTTACAGAGAT	127
Db	61	ATCTCTTAAGCTCGTGAATCTGCGCCGCGCTCGCGCTCCCAAGTGTGGGATTTACAGAGAT	120
QY	128	AGCCACTGCGCCCAAGCC	144
Db	121	AGCCACTGCGCCCAAGCC	137

RESULT 12	AA599141	LOCUS	DEFINITION
292 bp	AA599141	292 bp	linear
EST 06-MAR-199	aa52d07.s1	Stratagene lung carcinoma 937218 Homo sapiens cDNA clone	
IMAGE:950499_3		similar to contains Alu repetitive element:contains	
element XER40 repetitive element ;		mRNA sequence.	

ପ୍ରାୟ ୧୫

ORGANISM	Homo sapiens Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	NIH-MGC http://imgc.nci.nih.gov/ .
AUTHORS	1. (bases 1 to 507)
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
JOURNAL	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Dr. Michael Brownstein CDNA Library Preparation: Invitrogen Corp CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNU) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNU at: http://image.lnl.gov Plate: NDAW437 row: d column: 14 Library sequence stop: 507. High quality sequence location/Qualifiers
FEATURES	1..507 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:30375733" /tissue_type="White Matter" /dev_stage="Unknown" /lab_host="DH10B-TOP A (T1 and T5 phage resistances) " /clone_lib="NIH_MGC_181" /vector="PCMV-SPOK6.1; Site_1: NotI; Site_2: EcoRV (note: Vector: library is oligo-dT primed and directionally cloned (BCOV site is destroyed upon cloning). Average insert size 1.42 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC Library."
ORIGIN	Query Match 14.8%; Score 128.6; DB 14; Length 507; Best local Similarity 93.7%; Pred. No. 1,7e-14; Matches 134; Conservative 0; Mismatches 9; Indels 0; Gaps 0
CY	10 TTTTCTTTTTTTAGTAGAATGGGATTACCGGTAGCAGATGTCGAA 69
DB	505 TTTTCTTTTTTTTATGTAAGACGGGTTTCACTGTAGCAGATGTCGAA 446
CY	70 CTCTGACCTGTATCGCCCGCTCGACTGCCCTCCCAAGTGCTGGATTACAGCATAG 129
DB	445 CTCTGACCTGTATCACCCGCTCGACTGCCCTCCCAAGTGCTGGATTACAGCATAG 386
CY	130 CCATCGGCGCCAGCGGCTTT 152
DB	385 CCACCGCGCCAGCCATTTTT 363
RESULT 14	
BUE19183	647 bp mRNA linear EST 23-SEP-2001
LOCUS	UT-H-FRI-Bfr-k-19-0-U1.s1 NCI CGAP_FRI Homo sapiens cDNA clone
DEFINITION	UT-H-FRI-Bfr-k-19-0-U1 3', mRNA sequence.
ACCESSION	BUE19183
VERSION	BUE19183.1 GI:23285398
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1. (bases 1 to 647) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap . National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)
AUTHORS	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov
TITLE	Tissue Procurement: James Martin cDNA library preparation: D. W. Bento Soares, University of Iowa
JOURNAL	
COMMENT	

ORGANISM	Homo sapiens Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	NIH-MGC http://imgc.nci.nih.gov/ .
AUTHORS	1. (bases 1 to 507)
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
JOURNAL	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Dr. Michael Brownstein CDNA Library Preparation: Invitrogen Corp CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMU) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMU at: http://image.liml.gov Plate: NDM437 row: d column: 14 hitup sequence stopd: 507. location/Qualifiers
FEATURES	1..507 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:30375733" /tissue_type="White Matter" /dev_stage="Unknown" /lab_host="DH10B-TOP A (T1 and T5 phage resistances) " /clone_lib="NIH_MGC_181" /vector="PCMV-SPOK6.1; Site_1: NotI; Site_2: EcoRV (note): "Library is oligo-dT primed and directionally cloned (BCOV site is destroyed upon cloning). Average insert size 1.42 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC Library."
ORIGIN	Query Match 14.8%; Score 128.6; DB 14; Length 507; Best local Similarity 93.7%; Pred. No. 1,7e-14; Matches 134; Conservative 0; Mismatches 9; Indels 0; Gaps 0
Cy	10 TTTTTCCTTTTATGAGATGGGTACCGTGATGACAGATGCTCCGA 69
Ds	505 TTTTTCCTTTTATGAGATGGGTACCGTGATGACAGATGCTCCGA 446
Cy	70 CTCTGACTGTATCGCCGCTCGCCTCCCAAGTCTGGATTACAGCATAG 129
Ds	445 CTCTGACTGTATCGCCGCTCGCCTCCCAAGTCTGGATTACAGCATAG 386
Cy	130 CCATCGGCCCGACGCGCTTT 152
Ds	385 CCACCGGCCCGACGCAATTTTT 363
RESULT 14	
BUE19183	647 bp mRNA linear EST 23-SEP-2001
LOCUS	UT-H-FRI-Bfr-k-19-0-U s1 NCI CGAP_FRI Homo sapiens cDNA clone
DEFINITION	UT-H-FRI-Bfr-k-19-0-U1 3', mRNA sequence.
ACCESSION	BUE19183
VERSION	BUE19183.1 GI:23285398
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap . National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
AUTHORS	Unpublished (1997)
TITLE	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: James Martin cDNA library preparation: Dr. W. Bento Soares, University of Iowa
JOURNAL	
COMMENT	

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu
 The following repetitive elements were found in this cDNA
 sequence: 6-136 >NU (matched complement)
 Seq primer: M13 FORWARD
 POLYA=Yes.

FEATURES

source

1..647
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-FH1-bfn-k-19-0-UI"
 /tissue_type="Cell Line"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_id="NCI CGAP FH1"
 /note="Organ: Chondrosarcoma; Vector: pRT3-Pac
 (Pharmacia) with a modified polylinker; Site 1: EcoR I;
 Site 2: Not I; NCI CGAP FH1 is a normalized cDNA library
 obtained from a cell line derived from grade I
 chondrosarcoma tissue. The library was constructed and
 normalized according to Bonaldo, Lennon and Soares, Genome
 Research, 6:791-806, 1996. First strand cDNA synthesis was
 primed with an oligo-dT primer containing a Not I site.
 Double stranded cDNA was ligated to an EcoR I adaptor.
 digested with Not I, and cloned directionally into
 pRT3-Pac vector. The oligonucleotide used to prime the
 synthesis of first-strand cDNA contains a library tag
 sequence that is located between the Not I site and the
 (dT)18 tail. The sequence tag for this library is
 AGATCCGGC. The cell line was provided by Dr. James Martin
 from the University of Iowa.
 TAG: TISSUE=Human Chondrosarcoma Cell Line C88 - Grade 1
 Chondrosarcoma
 TAG_Lib=UI-H-FH1
 TAG_SEQ=AGATCCGGC"

ORIGIN

Query Match 14.8%; Score 128.6; DB 13; Length 647;
 Best Local Similarity 90.7%; Pred. No. 1.5e-14;
 Matches 137; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
 Oy 9 TTTTCTTTTCTTTTAAAGATGAGTGGGTTTACCGTGTAGCCAGATGGTCTCGA 68
 Db 1 TTTTCTTTTCTTTTAAAGATGAGTGGGTTTACCGTGTAGCCAGATGGTCTCGA 60
 Oy 69 ACTCTGACCTGCGATCGCCGCGCTTCCCAAGTCTGGATTCAGAGCATGA 128
 Db 61 TCTCTGACCTGCGATCGCCGCGCTTCCCAAGTCTGGATTCAGAGCATGA 120
 Oy 129 GCCACTGCGCCGCGGCTTTTAAACAT 159
 Db 121 GCCACGACGCCGCGGCTTTTAAACAT 151

RESULT 15
 BC041578 3538 bp mRNA linear HTC 19-NOV-2003
 LOCUS BC041578.1
 DEFINITION Homo sapiens hypothetical protein MGC17986, mRNA (cDNA clone
 IMAGE4640152), with apparent retained intron.
 ACCESSION BC041578
 VERSION BC041578.1 GI:27469657
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

TITLE
 JOURNAL MEDLINE
 PUBMED 12477932
 REFERENCE
 AUTHORS
 JOURNAL
 2 (bases 1 to 3538)
 Strausberg, R.
 Direct Submission
 Submitted (20-DEC-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgaps-remail.nih.gov
 Tissue Procurement: ATCC/DCMP/DBP
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLI)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc.mgc@nih.gov
 Akhtar, N., Ayte, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
 Hansen, N., Ho, S.-I., Karlins, E., Kwong, P., Leric, P., Iagasaki, R.,
 Maduoni, Q.L., Nasello, C., Maskell, B., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Stanclipp, S., Thomas, P.J., Touchman, J.W.,
 Young, A., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.

REMARK

COMMENT
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/ILNLI at: <http://image.llnl.gov>
 Series: IRAL Plate: 44 Row: e Column: 10
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 2357699
 This clone has the following problem: retained intron.
 Location/Qualifiers
 1..3538
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4640152"
 /tissue_type="Skin, melanotic melanoma."
 /clone_id="NIH-MGC 20"
 /lab_host="DH10B-R"
 /note="Vector: pOTB7"

FEATURES

source

1..3538
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4640152"
 /tissue_type="Skin, melanotic melanoma."
 /clone_id="NIH-MGC 20"
 /lab_host="DH10B-R"
 /note="Vector: pOTB7"

ORIGIN

Query Match 14.8%; Score 128.6; DB 11; Length 3538;
 Best Local Similarity 93.7%; Pred. No. 7.5e-15;
 Matches 134; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 Oy 9 TTTTCTTTTCTTTTAAAGATGAGTGGGTTTACCGTGTAGCCAGATGGTCTCGA 68
 Db 2222 TTTTCTTTTCTTTTAAAGATGAGTGGGTTTACCGTGTAGCCAGATGGTCTCGA 2163

Fri May 28 12:50:58 2004

us-10-621-363-12_1.rst

Page 10

QY 69 ACTCTGACCTCTGTGATCCGCCCGCCTCGGCTCCCAAGTGTGGATTACAGGCATGA 128
DB 2162 TCTCTGACCTGTGTGATCCGCCCGCCTCGGCTCCCAAGTGTGGATTACAGGCATGA 2103
QY 129 GCCACTGCGCGCCGAGCCGCTTT 151
DB 2102 GCCACCGCGGCGGCGAGGCTTT 2080

Search completed: May 24, 2004, 15:49:07
Job time : 2362 secs

www.bio.lnl.gov/bbrp/image/image.html
 Seq primer: -40UP from G1bco
 High quality sequence stop: 395.
 Location/Qualifiers
 1 491

FEATURES
 source
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:268447"
 /issue_type="serous papillary carcinoma, high grade, 2
 pooled tumors"
 /lab_host="DH10B"
 /clone_1lb="NCI CGAP Ut4"
 /note="Organ: Uterus; Vector: pCMV-Sport6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.48 Kb. Life Technologies catalog #:
 11542-016"

ORIGIN

Query Match 43.1%; Score 374; DB 10; Length 491;
 Best Local Similarity 100.0%; Pred. No. 3.8e-53;
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

19 TTTTAAAGTAGAGAGAGGAGGTTTCAACCGTGTAGCCAGAGATGCTCTCGAACTCTGACC 78
 1 TTTTAAAGTAGAGAGAGGAGGTTTCAACCGTGTAGCCAGAGATGCTCTCGAACTCTGACC 60
 79 TCGTATCCGCGCCCTCCGCTCCCAAGTGTGAGATTAAGAGCATGAGCCATGCGC 138
 61 TCGTATCCGCGCCCTCCGCTCCCAAGTGTGAGATTAAGAGCATGAGCCATGCGC 120
 139 CCAGCCGCTCTTTTAAACATTCGCCAGAGCTGTAGAGCAACCCATCTGACAT 198
 121 CCAGCCGCTCTTTTAAACATTCGCCAGAGCTGTAGAGCAACCCATCTGACAT 180
 199 TTGGAACTCCCGCCAGCCCATTAAGTGTGAGAGGTAAGAGCAAGAGAGAAAG 258
 181 TTGGAACTCCCGCCAGCCCATTAAGTGTGAGAGGTAAGAGCAAGAGAGAAAG 240
 259 GGGATTCACATCTAAGGTGTGATGCTGATGAGAGAGAGAGAGATCAGCAACAAA 318
 241 GGGATTCACATCTAAGGTGTGATGCTGATGAGAGAGAGAGAGATCAGCAACAAA 300
 319 GCGCTAGAGCTTTTAAACCAACACCTCTCTGCCACCTGCTTTGAAGGGGCAAA 378
 301 GCGCTAGAGCTTTTAAACCAACACCTCTCTGCCACCTGCTTTGAAGGGGCAAA 360
 379 GTATAGTGGCGAG 392
 361 GTATAGTGGCGAG 374

RESULT 2
 A1521901 421 bp mRNA linear EST 13-APR-1999
 LOCUS A1521901
 DEFINITION t180403.x1 NCI CGAP Kid1 Homo sapiens cDNA clone IMAGE:2138309 3'
 similar to contains Alu repetitive element; contains element PTRS
 repetitive element; mRNA sequence.

ACCESSION A1521901
 VERSION A1521901.1 GI:4436036
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 421)
 NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Straube, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lemmon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CCAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNLT at:
 www-bio.lnl.gov/bbrp/image/image.html
 Insert length: 718 Std Error: 0.00
 Seq primer: -40UP from G1bco
 High quality sequence stop: 401.
 Location/Qualifiers
 1 421

FEATURES
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2138309"
 /lab_host="DH10B"
 /clone_1lb="NCI CGAP Kid1"
 /note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with
 a modified polylinker; Site 1: Not I; Site 2: Eco RI;
 plasmid DNA from the normalized library NCI CGAP Kid3 was
 prepared, and as circles were made in vitro. Following RHP
 purification, this DNA was used as tracer in a subtractive
 hybridization reaction. The driver was PCR-amplified cDNAs
 from a pool of 5,000 clones made from the same library
 (cloneids 1323376-1323911, 1456007-1456775, and
 1500552-1502855). Subtraction by Bento Soares and M.
 Fatima Bonaldi."

ORIGIN

Query Match 42.8%; Score 371; DB 9; Length 421;
 Best Local Similarity 100.0%; Pred. No. 1.4e-52;
 Matches 371; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

22 TTTTAAAGTAGAGAGAGGTTTCAACCGTGTAGCCAGAGATGCTCTGAACTCTGACC 81
 1 TTTTAAAGTAGAGAGAGGTTTCAACCGTGTAGCCAGAGATGCTCTGAACTCTGACC 60
 82 TGAATCCGCGCCCTCCGCTCCCAAGTGTGAGATTAAGAGATGAGCCATGGGCCA 141
 61 TGAATCCGCGCCCTCCGCTCCCAAGTGTGAGATTAAGAGATGAGCCATGGGCCA 120
 142 GCGGCTCTTTTAAACATTCGCCAGAGCTGTAGAGCAACCCATCTGACATTTG 201
 121 GCGGCTCTTTTAAACATTCGCCAGAGCTGTAGAGCAACCCATCTGACATTTG 180
 202 GGAATCCGCGCCAGGCGCATTAAGTGTGAGAGGTAAGCAAGAGCAAGATGGGG 261
 181 GGAATCCGCGCCAGGCGCATTAAGTGTGAGAGGTAAGCAAGAGCAAGATGGGG 240
 262 GATTACACATCTAAGGTGTGATGCTGATGAGAGAGAGAGATCAGCGAACAAGCC 321
 241 GATTACACATCTAAGGTGTGATGCTGATGAGAGAGAGAGATCAGCGAACAAGCC 300
 322 TCTAGGTCTTTTAAACCAACACCTCTGACCACTGCTTTGAAGGGGCAAGTA 381
 301 TCTAGGTCTTTTAAACCAACACCTCTGACCACTGCTTTGAAGGGGCAAGTA 360
 382 TAGTGGCGAG 392
 361 TAGTGGCGAG 371

RESULT 3
 CA866165 527 bp mRNA linear EST 20-DEC-2002
 LOCUS CA866165
 DEFINITION t139406.x1 HR85 tset Homo sapiens cDNA clone IMAGE:5547308 3',
 mRNA sequence.
 ACCESSION CA866165
 VERSION CA866165.1 GI:27317714
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 527)
 Melton, D., Brown, J., Keny, G., Permut, A., Lee, C., Kaestner, K.,
 Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
 Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistein, A.,
 Schmitt, A., Theising, B., Ritter, B., Ronko, I., Bennett, J.,
 Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagaris, R.,
 Williams, T., Jackson, Y., and Bowers, Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
 Washington University Genome Sequencing Center For information on
 obtaining a clone please contact: Dr. Hiroshi Inoue
 (hinoue@im.wustl.edu)
 Seq primer: -40RP from Gldco
 High quality sequence stop: 450.
 Location/Qualifiers
 1..527
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6547308"
 /tissue_type="Purified pancreatic islet"
 /lab_host="DH10B"
 /clone_id="HR85 islet"
 /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
 NotI; Site_2: XhoI; DNA made by oligo-dT priming.
 Size-selected on agarose gel. Average insert size -1kb. 5'
 XhoI site was destroyed after directional cloning.
 Amplified once. Contact information: Hiroshi Inoue, MD,
 Metabolism Div. (Alan Permut Lab), Washington University
 School of Medicine, Box 8127, 660 South Euclid Ave., St.
 Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
 314-362-1916, Fax: 314-747-2692."

ORIGIN
 Query Match 42.8%; Score 371; DB 14; Length 527;
 Best Local Similarity 100.0%; Pred. No. 1,1e-52;
 Matches 371; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

22 TTTTAAGTAGAGAGGGGTTTACCGTGTAGCCAGAGTGGTCTCGAAGCTCGAGCTCG 81
 Db 1 TTTTAAGTAGAGAGGGGTTTACCGTGTAGCCAGAGTGGTCTCGAAGCTCGAGCTCG 60
 82 TGATCCGCCGCCCTCGGCTCTCCCAAGTGTCTGGATTACAGGCATGAGCCACTGCGCCA 141
 Db 61 TGATCCGCCGCCCTCGGCTCTCCCAAGTGTCTGGATTACAGGCATGAGCCACTGCGCCA 120
 142 GCGCGTCTTTTAAACATTCGCCAGAGTGTACAGCCAGCCATCTCAGCTGACATTTG 201
 Db 121 GCGCGTCTTTTAAACATTCGCCAGAGTGTACAGCCAGCCATCTCAGCTGACATTTG 180
 202 GGAATCCCCCGCCAGCCATTAAGTCTGACAGAGTGAAGACCAAGAGCAAGATGGG 261
 Db 181 GGAATCCCCCGCCAGCCATTAAGTCTGACAGAGTGAAGACCAAGAGCAAGATGGG 240
 262 GATTCACATCTAAGTCTGTGATGGCTGATGAAGAGAAAGATTCGCCAGCAAAAGCC 321
 Db 241 GATTCACATCTAAGTCTGTGATGGCTGATGAAGAGAAAGATTCGCCAGCAAAAGCC 300
 322 TCTAGGTCTTCTTACCAAAACACTCTCTGCGCCACTGCTTTGAAGAGGGGCGAAGTA 381
 Db 301 TCTAGGTCTTCTTACCAAAACACTCTCTGCGCCACTGCTTTGAAGAGGGGCGAAGTA 360

CA392561
 586 bp mRNA linear EST 06-NOV-2002
 cs26b04.y1 Human Retinal pigment epithelium/choroid cDNA
 (Un-normalized, unamplified): cs Homo sapiens cDNA clone cs26b04
 5', mRNA sequence.
 CA392561
 GI:24725399
 CA392561
 EST.
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 586)
 Wistow, G., Bernstein, S.L., Wyatt, M.K., Farris, R.N., Behal, A.,
 Touchman, J.W., Bouffard, G., Smith, D., and Peterson, K.
 Expressed sequence tag analysis of human RPE/choroid for the
 NEIBank Project: Over 6000 non-redundant transcripts, novel genes
 and splice variants
 Mol. Vis. 8 (4), 205-220 (2002)
 MEDLINE
 PUBMED
 12107410
 12107410
 Contact: Wistow G
 Section on Molecular Structure and Function
 National Eye Institute
 6/331, NIH, Bethesda, MD 20892-2740, USA
 Tel: 301 402 3452
 Fax: 301 496 0078
 Email: graeme@helix.nih.gov
 Plate: 26 row: b column: 04
 Seq primer: M13RP reverse primer (ABI).
 Location/Qualifiers
 1..586
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS26b04"
 /tissue_type="RPE/choroid"
 /dev_stage="Adult"
 /lab_host="EMDH10B"
 /clone_id="Human Retinal pigment epithelium/choroid cDNA
 (Un-normalized, unamplified): cs
 /note="Organ: Eye; Vector: pCMVSPORT6; Two different donor
 eyes (75-80 years old) yielded approximately 600 mg of
 dissected RPE/choroid tissue. This in turn yielded 340 ug
 of total RNA and 7 ug of mRNA. A directionally cloned cDNA
 library in the pCMVSPORT6 vector was constructed at life
 technologies (Rockville, MD; now part of Invitrogen Corp),
 essentially following the protocols of the Superscript
 Plasmid System (Invitrogen Corp).
 <http://www.invitrogen.com/>. The library code
 designation was cs. For this library, cDNA inserts were
 cloned into the NotI/Mlu sites of the vector. EST
 analysis was performed on the unamplified library at the
 NIH Intramural Sequencing Center (NISC)."

ORIGIN
 Query Match 42.2%; Score 366; DB 14; Length 586;
 Best Local Similarity 100.0%; Pred. No. 6,7e-52;
 Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

27 AGTAGAGATGGGTTTACCGTGTAGCCAGAGTGGTCTCGAAGCTCGAAGCTCGAGTGC 86
 Db 586 AGTAGAGATGGGTTTACCGTGTAGCCAGAGTGGTCTCGAAGCTCGAAGCTCGAGTGC 527
 87 CGCCCGCTCTGCGCTCCCAAGTGTCTGGATTACAGGCATGAGCCACTGCGCCAGCCGG 146
 Db 526 CGCCCGCTCTGCGCTCCCAAGTGTCTGGATTACAGGCATGAGCCACTGCGCCAGCCGG 467

QY 147 TTTTAAACATTTCCCGAGAGCTGTACAGCCACCATCTACCTGACATTTGGGAC 206
 DB 466 TCTTTTAAACATTTCCCGAGAGCTGTACAGCCACCATCTACCTGACATTTGGGAC 407
 QY 207 TCCCCCGAGAGCTGTACAGCCACCATCTACCTGACATTTGGGATTC 266
 DB 406 TCCCCCGAGAGCTGTACAGCCACCATCTACCTGACATTTGGGATTC 347
 QY 267 ACATCTAAGCTGTGTATGCTGTATGAAGAGAAATTCAGCAAAAGCTCTAG 326
 DB 346 ACATCTAAGCTGTGTATGCTGTATGAAGAGAAATTCAGCAAAAGCTCTAG 287
 QY 327 GTCTTTCTTACCAAAACACCTCTCTGCCCACCTGTTGAAGGGGGGAGATATAGG 386
 DB 286 GTCTTTCTTACCAAAACACCTCTCTGCCCACCTGTTGAAGGGGGGAGATATAGG 227
 QY 387 GGGGAG 392
 DB 226 GGGGAG 221
 RESULT 5 586 bp mRNA linear EST 06-NOV-2002
 CA392562/c 586 bp mRNA linear EST 06-NOV-2002
 LOCUS cs26b05.y1 Human Retinal pigment epithelium/choroid cDNA
 DEFINITION {un-normalized, unamplified}: cs Homo sapiens cDNA clone cs26b05
 5' mRNA sequence.
 ACCESSION CA392562 GI:24725401
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 586)
 Wistow, G., Bernstein, S.L., Wyatt, M.K., Ferris, R.N., Behal, A.,
 Touchman, J.W., Bouffard, G., Smith, D., and Peterson, K.
 Expressed sequence tag analysis of human RPE/choroid for the
 NIH Bank Project: Over 6000 non-redundant transcripts, novel genes
 and splice variants
 Mol. Vis. 8 (4), 205-220 (2002)
 22103460
 12107410
 COMMENT Contact: Wistow G
 Section on Molecular Structure and Function
 National Eye Institute
 6/331, NIH, Bethesda, MD 20892-2740, USA
 Tel: 301 402 3452
 Fax: 301 486 0078
 Email: grameewhelix.nih.gov
 Plate: 26 Row: b column: 05
 Seg primer: M13RP1 reverse primer (ABI).
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="cs26b05"
 /tissue_type="RPE/choroid"
 /dev_stage="Adult"
 /lab_host="EMD10B"
 /clone_lib="Human Retinal pigment epithelium/choroid cDNA
 (un-normalized, unamplified): cs"
 /note="Organ: Eye; Vector: pCMVSPORT6; Two different donor
 eyes (75-80 years old) yielded approximately 600 ng of
 dissected RPE/choroid tissue. This in turn yielded 340 ug
 of total RNA and 7 ug of mRNA. A directionally cloned cDNA
 library in the pCMVSPORT6 vector was constructed at Life
 Technologies (Rockville, MD; now part of Invitrogen Corp),
 essentially following the protocols of the Superscript
 Plasmid System (Invitrogen Corp).
 <http://www.invitrogen.com/>. The library code

ORIGIN
 Query Match 42.2%; Score 366; DB 14; Length 586;
 Best Local Similarity 100.0%; Pred. No. 6,7e-52;
 Matches 366; Conservative 0; Mismatches 0; Gaps 0;
 designation was cs. For this library, cDNA inserts were
 cloned into the NotI/MluI sites of the vector. EST
 analysis was performed on the unamplified library at the
 NIH Intramural Sequencing Center (NISC)."
 QY 27 AGTGAATGGGGTTTACCGTGTATACCAAGATGCTCTGAACTCTGACCTGTATC 86
 DB 586 AGTGAATGGGGTTTACCGTGTATACCAAGATGCTCTGAACTCTGACCTGTATC 527
 QY 87 CGCCGCGCTCGGCTCTCCCAAGATGCTGGATTACAGGATGAGCCACTGCGCCAGCGG 146
 DB 526 CGCCGCGCTCGGCTCTCCCAAGATGCTGGATTACAGGATGAGCCACTGCGCCAGCGG 467
 QY 147 TCTTTTAAACATTTCCCGAGAGCTGTACAGCCACCATCTACCTGACATTTGGGAC 206
 DB 466 TCTTTTAAACATTTCCCGAGAGCTGTACAGCCACCATCTACCTGACATTTGGGAC 407
 QY 207 TCCCCCGAGAGCTGTACAGCCACCATCTACCTGACATTTGGGATTC 266
 DB 406 TCCCCCGAGAGCTGTACAGCCACCATCTACCTGACATTTGGGATTC 347
 QY 267 ACATCTAAGCTGTGTATGCTGTATGAAGAGAAATTCAGCAAAAGCTCTAG 326
 DB 346 ACATCTAAGCTGTGTATGCTGTATGAAGAGAAATTCAGCAAAAGCTCTAG 287
 QY 327 GTCTTTCTTACCAAAACACCTCTCTGCCCACCTGTTGAAGGGGGGAGATATAGG 386
 DB 286 GTCTTTCTTACCAAAACACCTCTCTGCCCACCTGTTGAAGGGGGGAGATATAGG 227
 QY 387 GGGGAG 392
 DB 226 GGGGAG 221
 RESULT 6 941 bp mRNA linear EST 16-JUL-2002
 BQ710765/c 941 bp mRNA linear EST 16-JUL-2002
 LOCUS AGENCOURT 8484953 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301113
 DEFINITION 5' mRNA sequence.
 ACCESSION BQ710765 GI:21849664
 VERSION EST.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 941)
 NIH-MGC http://hgsc.ncl.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNU)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNU at:
 http://image.llnl.gov
 Plate: L10CM2516 row: h column: 10
 High quality sequence stop: 583.
 Location/Qualifiers
 1..941
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6301113"
 /lab_host="DH10B (phage-resistant)"

FEATURES

source

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 592)

Qian, B., Wu, T., Huang, Q., Kang, B., Gao, X., Xu, Z.,
Xiao, H., Xu, X., Li, N., Peng, Y., Liu, F., Qu, J., Song, H., Cheng, Z.,
Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M.,
Lu, G., Yang, Y., Gu, Y., Chen, Z., and Han, Z.

AUTHORS

TITLE

Homo sapiens cDNA GLC clones

JOURNAL

Unpublished (2000)

COMMENT

Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn

FEATURES

This clone is available at CHGC in Shanghai.
Location/Qualifiers

1..592

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="GLCCOR12"

/tissue_type="corresponding non cancerous liver tissue"

/dev_stage="Adult"

/lab_host="SOLR"

/clone_lib="GLC"

/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN

Query Match

8.8%; Score 76; DB 9; Length 592;

Best Local Similarity 100.0%; Pred. No. 0.00034;

Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ds

68 AACTCTGACCTGTATCCGCCCTCGGCTCCCAAGTCTGGATTACAGCATG 127
191 AACTCTGACCTGTATCCGCCCTCGGCTCCCAAGTCTGGATTACAGCATG 250

Qy

128 AGCCACTGCGCCGACG 143
251 AGCCACTGCGCCGACG 266

Ds

RESULT 12

AV719326

601 bp mRNA linear EST 16-OCT-2000

LOCUS

AV719326 GLC Homo sapiens cDNA clone GLCCNF05 5', mRNA sequence.

ACCESSION

AV719326

AV719326.1 GI:10816478

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Zeguang Han

Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

201203, P. R. China

Tel: 86-21-50801919(ex.45)

Fax: 86-21-50801922

Email: hanzg@chgc.sh.cn

This clone is available at CHGC in Shanghai.

Location/Qualifiers

1..601

FEATURES

Source

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="GLCCNF05"

/tissue_type="corresponding non cancerous liver tissue"

/dev_stage="Adult"

/lab_host="SOLR"

/clone_lib="GLC"

/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN

Query Match

8.8%; Score 76; DB 9; Length 601;

Best Local Similarity 100.0%; Pred. No. 0.00033;

Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ds

68 AACTCTGACCTGTATCCGCCCTCGGCTCCCAAGTCTGGATTACAGCATG 127
199 AACTCTGACCTGTATCCGCCCTCGGCTCCCAAGTCTGGATTACAGCATG 258

Qy

128 AGCCACTGCGCCGACG 143
259 AGCCACTGCGCCGACG 274

Ds

RESULT 13

AV720014

LOCUS

AV720014 GLC Homo sapiens cDNA clone GLCCNG04 5', mRNA sequence.

ACCESSION

AV720014

AV720014.1 GI:10817166

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Zeguang Han

Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

201203, P. R. China

Tel: 86-21-50801919(ex.45)

Fax: 86-21-50801922

Email: hanzg@chgc.sh.cn

This clone is available at CHGC in Shanghai.

Location/Qualifiers

1..604

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="GLCCNG04"

/tissue_type="corresponding non cancerous liver tissue"

/dev_stage="Adult"

/lab_host="SOLR"

/clone_lib="GLC"

/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN

Query Match

8.8%; Score 76; DB 9; Length 604;

Best Local Similarity 100.0%; Pred. No. 0.00033;

Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Ds

68 AACTCTGACCTGTATCCGCCCTCGGCTCCCAAGTCTGGATTACAGCATG 127
206 AACTCTGACCTGTATCCGCCCTCGGCTCCCAAGTCTGGATTACAGCATG 265

QY 128 AGCCACTGGCCGACC 143
 DB 266 AGCCACTGGCCGACC 281

RESULT 14
 AV720842 613 bp mRNA linear EST 16-OCT-2000
 LOCUS AV720842 GUC Homo sapiens cDNA clone GACCOH05 5', mRNA sequence.
 DEFINITION AV720842
 ACCESSION AV720842
 VERSION AV720842.1 GI:10817994
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 613)
 AUTHORS Qian, B., Wu, T., Huang, Q., Huang, C., Kang, B., Gao, X., Xu, Z., Xiao, H., Xu, X., Li, N., Peng, Y., Liu, F., Qu, J., Song, H., Cheng, Z., Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Yang, Y., Gu, Y., Chen, Z. and Han, Z.
 TITLE Homo sapiens cDNA GUC clones
 JOURNAL Unpublished (2000)
 COMMENT Chinese: Zengqiang Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China
 Tel: 86-21-50801919 (ex.45)
 Fax: 86-21-50801922
 Email: hanzg@hgc.sh.cn
 This clone is available at CHGC in Shanghai.

FEATURES
 source
 Location/Qualifiers
 1..613
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5739759"
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 /lab_host="DH10B (phage-resistant)"
 /clone_id="NTH MGC 88"
 /note="Organ: small intestine; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH-MGC Library."

ORIGIN
 Query Match 8.8%; Score 76; DB 9; Length 613;
 Best Local Similarity 100.0%; Pred. No. 0.00033; Indels 0; Gaps 0;
 Matches 76; Conservative 0; Mismatches 0;

QY 68 AACTCTGACCTCGTATCGCGCCGCTCGGCTCCCAAGTCTGGATTACAGGCATG 127
 DB 187 AACTCTGACCTCGTATCGCGCCGCTCGGCTCCCAAGTCTGGATTACAGGCATG 246

QY 128 AGCCACTGGCCGACC 143
 DB 247 AGCCACTGGCCGACC 262

RESULT 15
 BM561574 481 bp mRNA linear EST 20-FEB-2002
 LOCUS BM561574
 DEFINITION AGENCOURT_6567251 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5739759
 5', mRNA sequence.
 ACCESSION BM561574
 VERSION BM561574.1 GI:18806941
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 481)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov
 Plate: LHAM12753 row: j column: 16
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FEATURES
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 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5739759"
 /tissue_type="duodenal adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="NTH MGC 88"
 /note="Organ: small intestine; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH-MGC Library."

ORIGIN
 Query Match 8.5%; Score 74; DB 12; Length 481;
 Best Local Similarity 100.0%; Pred. No. 0.00088; Indels 0; Gaps 0;
 Matches 74; Conservative 0; Mismatches 0;

QY 60 TGGTCTGACCTCGTATCGCGCCGCTCGGCTCCCAAGTCTGGATTACAGGCATG 119
 DB 22 TGGTCTGACCTCGTATCGCGCCGCTCGGCTCCCAAGTCTGGATTACAGGCATG 81

QY 120 CAGGCTAGGCCAC 133
 DB 82 CAGGCTAGGCCAC 95

Search completed: May 24, 2004, 18:18:40
 Job time : 2344 secs

PR 19-AUG-1997; 97US-0056364D.
 PR 19-AUG-1997; 97US-0056365P.
 PR 19-AUG-1997; 97US-0056366P.
 PR 19-AUG-1997; 97US-0056367P.
 PR 19-AUG-1997; 97US-0056370P.
 PR 19-AUG-1997; 97US-0056371P.
 PR 19-AUG-1997; 97US-0056571P.
 PR 19-AUG-1997; 97US-0056573P.
 PR 19-AUG-1997; 97US-0056573P.
 PR 19-AUG-1997; 97US-0056731P.
 PR 19-AUG-1997; 97US-0056732P.
 PR 04-AUG-1998; 98MO-US016235.
 PR 04-FEB-1999; 99US-00244112.
 PR 06-OCT-2000; 2000US-0238291P.
 PR 01-FEB-2001; 2001US-00774639.
 XX
 PA (RUBEN/) RUBEN S. M.
 PA (SOPET/) SOPPET D. R.
 PA (EBNER/) EBNER R.
 PA (OLSEN/) OLSEN H. S.
 PA (YOUNG/) YOUNG P. E.
 PA (GREEN/) GREENE J. M.
 PA (FERRE/) FERRE A. M.
 PA (YU/) YU G.
 PA (NIU/) NI J.
 PA (ROSEN/) ROSEN C. A.
 PA (BREWER/) BREWER L. A.
 PA (JANAT F.)
 PA (BIRSE/) BIRSE C. E.
 XX
 PI Ruben SM, Soppet DR, Ebner R, Olsen HS, Young PE, Greene JM;
 PI Ferrie AM, Yu G, Ni J, Rosen CA, Brewer LA, Janat F, Birse CE;
 XX
 DR WPI: 2003-695903/66.
 DR P-PSDB; ADB47826.
 XX
 PT Novel human secreted proteins useful for treating and/or diagnosing
 PT disorders of immune system, cardiovascular disorders such as peripheral
 PT artery disease, neurological diseases such as Alzheimer's disease.
 XX
 PS Claim 3; Page 205; 333pp; English.
 XX
 CC The invention relates to novel human secreted proteins. The protein is
 CC useful for preventing, treating or ameliorating a medical condition. The
 CC protein is useful for diagnosing a pathological condition or
 CC susceptibility to a pathological condition in a subject. The protein is
 CC useful for identifying a binding partner. The nucleic acid is useful for
 CC diagnosing pathological condition or a susceptibility to pathological
 CC condition in a subject. The protein is useful as reagents for
 CC differential identification of the tissues or cell types present in a
 CC biological sample. The protein can be administered to patients having
 CC absent or decreased levels of polypeptides e.g. insulin, to supplement
 CC absent or decreased levels of different polypeptides, e.g. haemoglobin S
 CC for haemoglobin B, superoxide (SOD), catalase, DNA repair protein, to
 CC inhibit the activity of a polypeptide e.g. an oncogene or tumour
 CC suppressor, to activate the activity of polypeptide e.g. by binding to a
 CC receptor, to reduce the activity of membrane bound receptor by competing
 CC with it for free ligand e.g. soluble tumour necrosis factor (TNF)
 CC with it for free ligand e.g. soluble tumour necrosis factor (TNF)
 CC receptor used in reducing inflammation, or to bring about a desired
 CC response e.g. blood vessel growth inhibition, enhancement of immune
 CC response to proliferative cells or tissues. The protein and the nucleic
 CC acid are useful for treating, preventing, detecting, diagnosing disorders
 CC of immune system involving abnormal growth of specific types of cells as
 CC well as of other cell types where expression has been observed. The
 CC protein, the nucleic acid and antibodies are useful for treating,
 CC preventing and/or diagnosing diseases, disorders and/or conditions of
 CC immune system, hyperproliferative disorders including neoplasms,
 CC cardiovascular disorders (such as peripheral artery disease, limb
 CC ischaemia, arterio-arterial fistula, arteriovenous fistula, congenital
 CC heart defects, etc), neovascularisation disorders, wound healing and
 CC epithelial cell proliferation, neurological diseases (such as Alzheimer's
 CC disease, Parkinson's disease, Huntington's disease, mania, dementia,
 CC etc), infectious diseases caused by virus, bacteria, fungi, etc. The
 CC present sequence represents a cDNA encoding a novel human secreted

[illegible]

XX		26-MAR-2002; 2002MCO-US009370.
PF		
PR	27-MAR-2001; 2001US-0278650P.	
PR	12-SEP-2001; 2001US-00950082.	
PR	12-SEP-2001; 2001US-00950083.	
XX		
PA	(HOMA-) HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA, Ruben SM;	
XX		
DR	WPI; 2003-040578/03.	
PT	New human secreted proteins and nucleic acids, useful for detecting or	
PT	treating cancer or other hyperproliferative disorders, autoimmune	
PT	disorders, inflammatory disorders, HIV disease, hepatitis or anemia.	
XX		
PS	Disclosure; Page 2331-2345; 24749P; English.	
XX		
CC	ABZ73261-ABZ73697 represent cDNAs corresponding to 391 human secreted	
CC	protein genes, and ABP00947-ABP01363 represent the proteins they encode.	
CC	ABZ73698-ABZ74687 represent human secreted protein genomic fragments. The	
CC	invention also encompasses antibodies specific for the secreted proteins,	
CC	the use of the secreted proteins in drug screening and recombinant	
CC	vectors and host cells comprising a nucleic acid of the invention. The	
CC	secreted proteins are thought to be involved in biological activities	
CC	associated with cellular signaling, cellular differentiation, cell	
CC	migration, prohomeostatic activation and neurotransmitter activity. The	
CC	secreted proteins, nucleic acids encoding them, antibodies or antibody	
CC	fragments specific for the secreted proteins, and modulators of protein	
CC	activity are useful for diagnosing or treating cancers or other	
CC	hyperproliferative disorders. Additionally, the secreted proteins and	
CC	their nucleic acids may also be used in the treatment of autoimmune	
CC	disorders, inflammatory disorders, diseases involving angiogenesis, AIDS	
CC	(acquired immunodeficiency syndrome), hepatitis, anaemia, and to promote	
CC	wound healing. Nucleic acids of the invention may be used for chromosome	
CC	identification, chromosome mapping, in gene therapy, for identifying	
CC	individuals from minute biological samples, as hybridisation probes, and	
CC	as molecular weight markers. The present sequence represents a human	
CC	secreted protein genomic fragment referred to in the disclosure of the	
CC	invention	
SQ	Sequence 58181 B?; 15503 A; 12755 C; 13504 G; 16419 T; 0 U; 0 Other;	
Query Match	94.9%; Score 822.6; DB 7; Length 58181;	
Best Local Similarity	99.3%; Pred. No. 6.2e-224;	
Matches 844; Conservative	2; Mismatches 2; Indels 2; Gaps 2;	
OY	6 TTTTYYYYTTTTTTTTTAAGTAGAATGGGATTACCGTGTTNCCAGAGATSGTCT 65	
Db	52565 TTTTTTTTTTTTTTTTTTAAGTAGAATGGGATTACCGTGTTNCCAGAGATSGTCT 52508	
OY	66 CGAACTCTGTACCTCTGTATCCGCCGCCTTCGCCCAAAATGCTGGATTAACAGGA 125	
Db	52505 CGAACTCTGTACCTCTGTATCCGCCGCCTTCGCCCAAAATGCTGGATTAACAGGA 52446	
OY	126 TGAGCACAATGCGCCAGCGGATCTTTTAAACATTTCCCAGACTGTACAGCCACCAT 185	
Db	52445 TGAGCACAATGCGCCAGCGGATCTTTTAAACATTTCCCAGACTGTACAGCCACCAT 52386	
OY	186 ACTGACTGACATTTGGGAATCCCCCCCAAGCCATACTGATCTGCAAGGTAAAGCC 245	
Db	52385 ACTGACTGACATTTGGGAATCCCCCCCAAGCCATACTGATCTGCAAGGTAAAGCC 52322	
OY	246 AAGGCAAGAATGGGGGATTCACATCTAAAGTCTGTGATAGGCTGAAGAAGAAAGAA 305	
Db	52325 AAGGCAAGAATGGGGGATTCACATCTAAAGTCTGTGATAGGCTGAAGAAGAAAGAA 52266	
OY	306 TCAGGGAACAAGACTCTAGTCTTTTCTTAACAACAACCTCTGCGCACCTGCTTT 365	
Db	52265 TCAGGGAACAAGACTCTAGTCTTTTCTTAACAACAACCTCTGCGCACCTGCTTT 52206	
OY	366 GAAGGGGCAAGAATATGATGGAGGA-GCTGCCACCTGTCTACAGTGAAGGATCTGGAG 424	

Db	52205	GAAGGGGACAGAAAGTAATAGTGGGCGAGGGTGGCCCACTGCTCAAGTGAAGGATCTGAG	52146
Qy	425	AAATACTCAACTTTTGAGGTGCTCGCCCTCTTCATAGCAGACTCTAACTTAAGCCAATG	484
Db	52145	AAATATCTCAACATTTGAGGTGCTCGCCCTCTTCATAGCAGACTCTAACTTAAGCCAATG	52086
Qy	485	ACCCACGAGAG-CTTACACAAATTCMAACAGGCGCCAAATGATTCATAGCAGGGGAG	543
Db	52085	ACCCACGAGAGGCTTACACAAATTCMAACAGGCGCCAAATGATTCATAGCAGGGGAG	52026
Qy	544	GCCAAAGACTCCGAGAGAGAGAGGCCCAATAGGCTGGTGTATTTCCGATCCATAGAG	603
Db	52025	GCCAAAGACTCCGAGAGAGAGAGGCCCAATAGGCTGGTGTATTTCCGATCCATAGAG	51966
Qy	604	AGAGCAGAGGTGGGCGAGGCCCTTTGATTAAATGATTCATTTCTGAATGCAACTTCAAA	663
Db	51965	AGAGCAGAGGTGGGCGAGGCCCTTTGATTAAATGATTCATTTCTGAATGCAACTTCAAA	51906
Qy	664	TCCGGGTATGCGCGGTGAGAAATGAGACGACTTAACTCGGTGTATGCGCAAGCTCCA	723
Db	51905	TCCGGGTATGCGCGGTGAGAAATGAGACGACTTAACTCGGTGTATGCGCAAGCTCCA	51848
Qy	724	GCGCCGACTGCGCCGAGAGACAGATCCGCCAAGAGGCTGTGAGAGGCTGTGGCCAGCC	783
Db	51845	GCGCCGACTGCGCCGAGAGACAGATCCGCCAAGAGGCTGTGAGAGGCTGTGGCCAGCC	51786
Qy	784	ACTCGATTTTAAACCCCGGCTCCTCAAGGTCAAGCTGTGAGCCTTGANTGAACACTTC	843
Db	51785	ACTCGATTTTAAACCCCGGCTCCTCAAGGTCAAGCTGTGAGCCTTGANTGAACACTTC	51726
Qy	844	TATGACCAAT 853	
Db	51725	TATGACCAAT 51716	
RESULT 5			
ADC21010/c			
ADC21010 standard; DNA; 58181 BP.			
AC	ADC21010;		
DT	18-DEC-2003 (first entry)		
DE	Human secreted protein-related DNA sequence #428.		
XX	gene therapy; human; secreted protein; haemopoietic disorder;		
KM	haematological disorder; anaemia; haemophilia; inflammatory disorder;		
KM	haematological disorder; anaemia; haemophilia; inflammatory disorder;		
KM	inflammatory bowel disease; Crohn's disease; neoplastic disease; cancer;		
KM	leukaemia; wound healing; epithelial cell proliferation disorder;		
KM	immune disorder; autoimmune disorder; asthmatic disorder;		
KM	cardiovascular disorder; atherosclerosis; myocarditis;		
KM	infectious disease; HIV; AIDS; endocrine disorder; diabetes;		
KM	gastrointestinal disorder; duodenal ulcer; gastroenteritis; gene; de.		
XX			
OS	Homo sapiens.		
XX			
PM	MO200292787-A2.		
PD	21-NOV-2002.		
XX			
PF	26-MAR-2002; 2002MCO-US009257.		
XX			
PR	27-MAR-2001; 2001US-0278650P.		
PR	12-SEP-2001; 2001US-00950082.		
PR	12-SEP-2001; 2001US-00950083.		
XX			
PA	(HUMA-) HUMAN GENOME SCI INC.		
XX			
P1	Rosen CA, Ruben SM;		
DR	WPI; 2003-129287/12.		
XX			
PT	New human secreted proteins and nucleic acid molecules, useful for		

XX	Lees AM, Lees RS, Law SW, Arjona AA;
XX	MP1; 2001-565505/63.
DR	P-P8DB; AAB82809.
XX	
PT	New isolated low density lipoprotein binding polypeptide for treating,
PT	diagnosing and/or identifying therapeutic agents for atherosclerosis.
XX	
PS	Example 4; Fig 24; 143pp: English.
XX	
CC	The present sequence is that of genomic DNA encoding novel human low
CC	density lipoprotein binding protein 3 (LBP-3, see AAB82809). The DNA was
CC	isolated from a human genomic library by screening with LBP-3 cDNA (see
CC	AAB26501). The open reading frame spans 10 exons. Human LBP-2 nucleic
CC	acids are among claimed polymucleotides of the invention that encode
CC	novel polypeptides, termed LBPs, capable of binding to native and
CC	methylated LDL. Also claimed are isolated LBP polypeptides, and
CC	biologically active fragments and analogues of them, as well as
CC	expression vectors, cells and methods of producing the LBPs. Methods of
CC	determining if an animal is at risk for atherosclerosis, methods for
CC	evaluating an agent for use in treating atherosclerosis, and methods for
CC	treating a cell having an abnormality in structure or metabolism of LBP
CC	are claimed. Pharmaceutical compositions comprising also LBP polypeptide or
CC	nucleic acid, and vaccine compositions, are also claimed
XX	
SQ	Sequence 22255 BP; 5195 A; 5302 C; 5924 G; 5834 T; 0 U; 0 Other;
Query Match	15.0%; Score 110.4; DB 5; Length 22255;
Best Local Similarity	89.7%; Pred. No. 1.1e-27;
Matches 140; Conservative	0; Mismatches 16; Indels 0; Gaps 0;
YY	6 TTTTITTTTTTTTTTTTTTAAGTAGAGATGGGCTTTACCGCTGTAGCCAGAGTGCT 65
Dd	7346 TTTTITTTTTTTTTTTTTTTTGTAGAGACGGGGTTTCACCGTGTAGCCAGAGTGCT 7405
YY	66 CGAATCCTCGACTCGTGATTCGCCCGGCTCGGCCTCCCAAGTGTGGGATTACAGGA 125
Dd	7406 CGATCTCTTGACTCGTGATTCGCCCGGCTCGGCCTCCCAAGTGTGGGATTACAGCT 7465
YY	126 TGAGCACATCGCCGCCAGCCGGCTCTTTTAAACATTC 161
Dd	7466 TGAGCACACACCGCTGCTAATTATTTATTATTC 7501
Db	
RESULT 9	
ID	ACD13448
ID	ACD13448 standard; DNA; 115756 BP.
XX	
AC	ACD13448;
XX	
DT	13-AUG-2003 (first entry)
XX	
DE	Human DNA encoding a p53 modifier, SEQ ID 68.
XX	
KW	Human; ds; gene; p53 modifier; cytosolic; cancer; cytostatic;
KW	antitumorigenic; antiapoptotic; p53 pathway; breast cancer; colon cancer;
KW	kidney cancer; lung cancer; ovarian cancer; angiogenesis; cell cycle;
XX	apoptotic disorder; cell proliferation disorder.
OS	Homo sapiens.
PN	WO200299122-A1.
PD	12-DEC-2002.
PF	03-JUN-2002; 2002WO-US017382.
PR	05-JUN-2001; 2001US-0296076P.
PR	10-OCT-2001; 2001US-0328605P.
PR	15-FEB-2002; 2002US-0357253P.
PA	(EXEL-) EXELIXIS INC.

PI Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP,
 XX WPI: 2003-156859/15.
 DR P-PSDB; ABO07223.
 XX
 PT Identifying modulators of the p53 pathway for use in treating apoptotic
 PT or cell proliferation disorders, comprises screening for agents that
 PT modulate activity of a human ortholog of genes that modify the p53
 PT pathway in Drosophila.
 XX
 XX Example 2: Page 320-351; 678pp; English.
 XX
 CC The invention relates to identifying (M1) a candidate p53 pathway
 CC modulating agent, by contacting an assay system comprising a purified HM
 CC polypeptide (human orthologue of genes that modify the p53 pathway in
 CC Drosophila) or nucleic acid with a test agent under conditions, where but
 CC for the presence of the test agent, the system provides a reference
 CC activity, and detecting a test agent-biased activity of the assay system.
 CC Also included are modulating (M2) a p53 pathway of a cell (comprising
 CC contacting a cell defective in p53 function with a candidate modulator
 CC that specifically binds to an HM polypeptide comprising an HM amino acid
 CC sequence, where p53 function is restored), modulating (M3) a p53 pathway
 CC in a mammalian cell (comprising contacting the cell with an agent that
 CC specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4)
 CC a disease in a patient (comprising: (a) obtaining a biological sample
 CC from the patient; (b) contacting the sample with a probe for HM
 CC expression; (c) comparing the results with a control; and (d) determining
 CC whether the comparison indicates a likelihood of disease). (M1) is useful
 CC for identifying modulators of the p53 pathway. A probe for HM expression
 CC is useful for diagnosing breast, colon, kidney, lung and ovarian cancer,
 CC in a patient, where the cancer has greater than 25 % expression level.
 CC Modulators identified by (M1) are useful in a variety of diagnostic and
 CC therapeutic applications, where disease or disorder prognosis is related
 CC to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell
 CC proliferation disorders (e.g. cancer). Another two new methods (M2 and
 CC M3) are useful for modulating the p53 pathway of a cell, thus restoring
 CC the p53 function of the cell, so that the cell undergoes normal
 CC proliferation or progression through the cell cycle. (M2) and (M3) are
 CC also useful for treating defects in the p53 pathway such as angiogenic,
 CC apoptotic or cell proliferation disorders. The present sequence is an HM
 CC nucleic acid encoding a p53 pathway modifying protein
 XX
 XX Sequence 115756 BP; 29575 A; 26665 C; 27977 G; 31539 T; 0 U; 0 Other;
 SQ
 Query Match 15.0%; Score 130.4; DB 7; Length 115756;
 Best Local Similarity 89.7%; Pred. No. 2.1e-27;
 Matches 140; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
 QY 6 TTTTCTTTTCTTTTCTTTTAAAGTAGAGGGGCTTACCCGGTTAGCCAGGAGAGTCT 65
 DB 74889 TTTTCTTTTCTTTTCTTTTAAAGTAGAGGGGCTTACCCGGTTAGCCAGGAGAGTCT 74948
 QY 66 CGAATCTCTGACCTCGTAGATCCGCCCGCTCGAGCTCCCAAGATGCTGAGATTACAGGCA 125
 DB 74949 CGATCTCTGACCTCGTAGATCCGCCCGCTCGAGCTCCCAAGATGCTGAGATTACAGGCT 75008
 QY 126 TTAGGCACTGGGCCCAAGCCGCTCTTTTAAACATTC 161
 DB 75009 TTAGGCACTGGGCCCAAGCCGCTCTTTTAAATTAATTC 75044
 RESULT 10
 AAL53468/c
 ID AAL53468 standard; DNA; 20951 BP.
 XX AAL53468;
 AC
 XX 16-JAN-2003 (first entry)
 DT
 XX Genomic DNA encoding human Ras-1like protein.
 DE
 XX Human; Anti-HIV; neuroprotective; antitropic; cerebroprotective; cardiatic;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (sites)
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
Isewura,M., Ikegawa,S., Kinjo,T. and Nakamura,Y.
DNA sequence analysis of a 1.9-Mb region on chromosome 8p11.2
Published Only in Database (1999)

2 (bases 1 to 100000)
Hitakawa,M., Yamaguchi,H., Inai,K. and Shimada,J.
Direct Submission
Submitted (12-FEB-1999) Mika Hitakawa, Japan Science and Technology Corporation (JST), Advanced Database Department, 5-3, Yonban-cho, Chiyoda-ku, Tokyo 102-0028, Japan (E-mail:mika@tokyo.jst.go.jp,
Tel:+81-3-5214-8491, Fax:+81-3-5214-8470)
This sequence is conducted by Japanese Foundation for Cancer Research as a JST sequencing team.
Principal Investigator: Yusuke Nakamura Ph.D
Phone:+81-3-5449-5372, Fax:+81-3-5449-5433.
yusuke@jgc.iins.u-tokyo.ac.jp
The sequence is submitted by Human Genome Sequencing in ALIS project of JST
Japan Science and Technology Corporation (JST)
5-3, Yonbancho, Chiyoda-ku, Tokyo, 102-0028 Japan
For further information about this sequences, please visit our
sequence archive web site (<http://www-alis.tokyo.jst.go.jp/HGS/top.html>) or send email to webmaster@www-alis.tokyo.jst.go.jp.

FEATURES
source
1..100000
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="8"
/map="8p11.2"

ORIGIN
Query Match 15.4%; Score 133.6; DB 9; Length 100000;
Best Local Similarity 76.9%; Pred.No.3.2e-29;
Matches 163; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Db 12 TTTT TTTT TTTT TTTT TAAGTAGAGATGGG GTTCACCGGTGTAAGCCAGATAGTGCTCCAACT 71
72336 TTTTTTTGTATT TTATTTAAGTAGAGAGCGGGTTTACCGGTGTAAGCCAGATAGTGCTCCACT 72499

Db 72 CCTGACCTCGATGC CGGCCGCGCCTCGGCTCCCAAGTGTGGATTTACAGGATGAAGCC 131
72496 CCGACCTCGATGC CGGCCGCGCCTCGGCTCCCAAGTGTGGATTTACAGGATGAAGCC 72555

Db 132 ACTGCGCCCGACCGCGGTCTTTTAAACAATCCCGCAGACTGTATACAGCAACCCTACTCAC 191
72556 ACCACGCCCGCGCTCATATTTTCATGATGCTAGAGGCAAGAATAAGTTGAACACTGTAA 72615

Db 192 CTGACATTGTGGAACTCCCCCCCACGGCCATA 223
72616 CTAACTATGTGGATATCTCACCATTGTCAAA 72647

LOCUS BX000688/c 102584 bp DNA linear PRI 24-JUN-2003
DEFINITION Human DNA sequence from clone DMOB-36F16 on chromosome 6, complete
sequence.
VERSION BX000688
KEYWORDS BX000688.11 GI:32187946
HTG
ORGANISM Homo sapiens (human)
REFERENCES
AUTHORS Submitted (24-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgehire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jun 24, 2003 this sequence version replaced gi:32186690.

COMMENT

```

----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk

-----
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YC.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Bm, EMBL, Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs constructed by
the HNC HaploType Consortium and collaborators. Further information
can be found at
http://www.sanger.ac.uk/HGP/Chn6/MHC
DNA8-36P16 is from a DNA-arcs QBL human bac library VECTOR:
pelobAC11.

Location/Qualifiers
1. 102684
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   /db_xref="taxon:9606"
   /chromosome="6"
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ORIGIN
Query Match          15.4%; Score 133.6; DB 9; Length 102684;
Best Local Similarity 93.8%; Pstd. No. 3.2e-29;
Matches 139; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY      6 TTTTCTTTTTTTTTTTTAAGTAGAGATGGGCTTCACCGGTAGCCAGGATGCTCT 65
Db      84698 TTTTCTTTTTTTTTTTTAAAGTAGAGAGGGGATTACCGATTAGCCAGATGACTCT 84633
QY      66 CGAAGCTCTGACCTCGTGATCGGCCGCCTCGGCTCCCAAGTGTGAGATTACAGGCA 125
Db      84638 CGAAGCTCTGACCTCGTGATCGGCCGCCTCGGCTCCCAAGATGCTGAGATTACAGGCG 84578
QY      126 TGAGGCCATGCGGCCCAAGCCGCTCTTTT 153
Db      84578 TGAGGCCATGCGGCCCAAGCCCTTTTITTT 84551

ACCO06137       129806 bp    DNA         linear     PRI 19-OCT-2001
LOCUS           AC006137
DEFINITION      Homo sapiens clone SCB-254N2 (UWGC:rg254N02) from 6p21, complete
sequence.
ACCESSION       AC006137
VERSION         AC006137.3   GI:16271961
KEYWORDS        HTG.
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 129806)
Janczyk, M., Guillaudoux, T., Vu, Q., Kutayavin, T., Harter, H. and
Geraghty, D.E.
```


Fri May 28 12:50:57 2004

us-10-621-363-12_1.rge

Page 7

ACCESSION AL031983
 VERSION AL031983.2 GI:12329558
 KEYWORDS HTG; CpG island; diubiquitin; GABBR1; olfactory receptor; OR2H2;
 OR2H5P; OR21P; RPL13A; SMT3H1; SMT3H2.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 134292)
 AUTHORS Younger,R.
 TITLE Direct Submission
 JOURNAL Submitted (20-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
 COMMENT requests: clonerequests@sanger.ac.uk
 On Jan 21, 2001 this sequence version replaced gi:4160199.

during sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; SW: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone cortigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/6p/Chr6>

Rp1-271M21 is from the library RPc1-1 constructed by the group of Pieter de Jong. for further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pCYPAC2

chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. IMPORTANT: This sequence is not the entire insert of clone Rpl-271M21. It may be shorter because we sequence overlapping sections only once, excepting for a 100 base overlap. The true left end of clone Rpl-271M21 is at 134292 in this sequence. The true right end of clone Rpl-271M21 is at 1 in this sequence.

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FEATURES
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    7857. .8024
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    /note="11M4 repeat: matches 3415. .3586 of consensus"
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repeat_region	14700. .14834
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repeat_region	30633. .30690

TITLE
JOURNAL
Submitted (12-DEC-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 164872)
REFERENCE
AUTHORS
Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barina, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouckgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, P., Cooke, P., Dekrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Gird, S., Graham, L., Grand, P., Hafez, N., Hages, B., Horton, L., Hulme, W., Iller, I., Johnson, R., Jones, C., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrum, J., Meneus, L., Mhova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupack, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE
JOURNAL
Submitted (15-JAN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 164872)
REFERENCE
AUTHORS
Birren, B., Nusbaum, C., Lander, E., Abouelella, A., Allen, N., Anderson, S., Arachchi, H.M., Barina, N., Bastien, V., Bloom, T., Boguslavsky, L., Bouckgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Cornu, B., Dekrellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand, P., Hulme, W., Hafez, N., Hageplan, D., Hages, B., Hall, J., Horton, L., Hulme, W., Iller, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrum, J., Meneus, L., Mhova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Ramchuka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupack, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, K., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataratan, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE
JOURNAL
Submitted (26-FEB-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 26, 2003 this sequence version replaced gi:2753762.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
COMMENT
Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Project information
Center project name: L28708
Center clone name: 1147_M_13

FEATURES

source

Location/Qualifiers
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Qy      192  CTGACATTTGGGAAGTCCCGCCCGACGCGGCATA 223
Db      35971 CTAAACATGTGGAGATATCTCACCATTTGGTCAAA 36002
    
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Search completed: May 24, 2004, 15:09:30
 Job time : 2506 secs

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 ESASOOLEERONKLEKLEBELLEBEGGNNEMASDRVAKATQOEOLNLELATERSTQON
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ORIGIN

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 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 AGTGAAGATGGGGTTTCAACCGTGTAGCCAGATGCTCGAATCTCTGACCTTCGATC 86
 DB 38600 AGTGAAGATGGGGTTTCAACCGTGTAGCCAGATGCTCGAATCTCTGACCTTCGATC 38541
 QY 87 CGCCCGGCTCGGCTCCCAAGTCTGGGATTTACAGGC 124
 DB 38540 CGCCCGGCTCGGCTCCCAAGTCTGGGATTTACAGGC 38503

RESULT 8
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 LOCUS Pan troglodytes chromosome 22 clone:RP43-038C12, map 22, complete
 DEFINITION
 ACCESSION BS000050
 VERSION BS000050.1 GI:37537317
 KEYWORDS HTG.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.

REFERENCE 1
 AUTHORS The Chimpanzee Chromosome 22 Sequencing Consortium.
 TITLE DNA sequence of chimpanzee chromosome 22 and its evolutionary
 JOURNAL implications
 REFERENCE 2 (bases 1 to 202014)
 AUTHORS Hattori,M., Toyoda,A., Watanabe,H., Taylor,T.D., Kuroki,Y.,
 Fujiyama,A. and Sakaki,Y.
 TITLE Direct Submission
 JOURNAL Submitted (12-MAY-2003) Masahira Hattori, The Institute of Physical
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
 1-7-22 Suehiro-chou,Tsukumi-Ku, Yokohama, Kanagawa 230-0045, Japan
 (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,

COMMENT

Tel:81-45-503-9111, Fax:81-45-503-9170)
 *The Chimpanzee Chromosome 22 Sequencing Consortium consists of:
 *Chinese National Human Genome Center at Shanghai, Shanghai, China;
 *GSC, Dept. of Genome Analysis, Braunschweig, Germany; *Institute
 of Molecular Biotechnology, Jena, Germany; *KRISS Genome Research
 Center, Daejeon, Korea;
 *Max-Planck-Institute for Molecular Genetics, Berlin, Germany;
 *National Institute of Genetics, Mishima, Japan;
 *National Yang Ming University Genome Research Center, Taipei,
 Taiwan;
 *RIKEN Genomic Sciences Center, Yokohama, Japan.

 Center: RIKEN Genomic Sciences Center
 Center code: RIKEN
 Web site: http://hgp.gsc.riken.go.jp/
 Contact: hattori@gsc.riken.go.jp

 Project Information
 Center project name: The Chimpanzee Chromosome 22 Sequencing Project
 Center clone name: RP43-038C12

 Sequencing Vector: pUC18, pUC13, pTZ19R, 100% of reads Chemistry:
 Dye-terminator Big Dye and ET; 100% of reads Assembly program:
 Phrap; version 0.990329
 Consensus quality: 200,900 bases at least Q40
 Consensus quality: 633 bases at least Q30
 Consensus quality: 83 bases at least Q20

This sequence was finished as follows unless otherwise noted: all
 regions were double stranded, sequenced with an alternate
 chemistry, or covered by high quality data (i.e., phred quality >=
 30);
 an attempt was made to resolve all sequencing problems, such as
 compressions and repeats; all regions were covered by at one
 plasmid
 subclone or more than one M13 subclone;
 and the assembly was confirmed by restriction digest.

Source information:

The RP43-43 chimpanzee BAC library was prepared from DNA isolated
 from the blood of a single male chimpanzee using published
 protocols (Osoegawa, K. et al. Genomics 52:1-8). The DNA from the
 chimpanzee ('Clint') was obtained from the Yerkes Primate Center in
 Atlanta. The library was prepared by Baoli Zhu, Chung Li Shu,
 Kazuhiro Osoegawa, Evan Eichler & Pieter J de Jong. The library
 characteristics are described at
 http://www.choi.org/bacpac/mchimp43.htm.
 The clone may be obtained from Pieter J. de Jong and coworkers
 (http://www.choi.org/bacpac).
 VECTOR: pBAC3.6

The CHORI-251 chimpanzee BAC library was prepared from DNA isolated
 from the blood of a single male chimpanzee using published
 protocols (Osoegawa, K. et al. Genomics 52:1-8). The DNA from the
 chimpanzee ('Clint') was obtained from the Yerkes Primate Center in
 Atlanta. The library was prepared by Baoli Zhu, Chung Li Shu,
 Kazuhiro Osoegawa, Evan Eichler & Pieter J de Jong. The library
 characteristics are described at
 http://www.choi.org/bacpac/chimpanzee251.htm.
 The clone may be obtained from Pieter J. de Jong and coworkers
 (http://www.choi.org/bacpac).
 VECTOR: pPRBAC2.1

The PTB1 chimpanzee BAC library was prepared from DNA isolated from
 cultured cells established from the blood of a single male
 chimpanzee.

Clones may be obtained from Asao Fujiyama and co-workers
 (http://www.gsc.riken.go.jp).
 VECTOR: pGS145

The PTF22 chimpanzee Fosmid library was prepared from DNA isolated
 from cultured cells established from the blood of a single male
 chimpanzee.

Clones may be obtained from Asao Fujiyama and co-workers
 (http://www.gsc.riken.go.jp).
 VECTOR: pKS143

Sequence Quality Assessment:
This entry has been annotated with sequence estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.

Neighboring clones: RP43-069C10(left) and RP43-089B14(right).

FEATURES

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ORIGIN

Query Match 11.3%; Score 98; DB 9; Length 202014;
Best Local Similarity 100.0%; Pred. No. 6,4e+46;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

27 AGTAGAGATGGGGTTTTCACCGTGTACCGAGATGCTCGAATCTCTGACCTCGTGCATC 86
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87 CGCCCGCCTCGGCTCCCAAGTCTCGGATTACAGGC 124
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90964 CGCCCGCCTCGGCTCCCAAGTCTCGGATTACAGGC 90927

RESULT 9
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LOCUS Homo sapiens 3 BAC RP11-85A3 (Roswell Park Cancer Institute Human

DEFINITION BAC library) complete sequence.

AC021026 GI:22002087

HTG.

Homo sapiens (human)

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 75555)
Mazny,D.M., Adams,C., Adio-Ogunola,B., Ali-osman,F.R., Allen,C.,
Alshrooke,S.L., Amaralunga,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbata,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,R., Brown,M., Bryant,N.P.,
Buhay,C., Burck,P., Burkelt,C., Cavazos,S.R., Chacko,J., Chavez,D.,
Carton,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dahorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
DeLaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Ehrhart,C., Eger,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falis,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Franz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,M., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., He,X.,
Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,
Hollins,B., Homel,P., Howard,S., Huber,J., Hulik,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudan,S., Karlsson,E., Kelly,S., Khan,U., King,J., Kovach,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,J.C.,
Lewis,L., Li,J., Li,Z., Licharge,O., Lien,C., Liu,J., Liu,M.,
Louisgess,H., Lozano,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhinney,B., McLeod,M.P., Meador,M.,
Mei,G., Metzger,M., Miner,G., Miner,Z., Mitchell,T., Mohabadi,K.,
Moore,S., Morgan,M., Moorish,T., Morris,S., Moser,M., Neal,D.,
Nelson,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N.,
Nickerson,E., Nwokenwo,S., Oghu,M., Okunolu,G., Oregunye,N.,

TITLE

JOURNAL

AUTHORS

REFERENCE

TITLE

JOURNAL

AUTHORS

REFERENCE

COMMENT

Ovidio, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L.,
Picerno, R., Priamus, E., Pu, L., Quiles, M., Ren, Y., Rivers, M.,
Rojas, A., Rojokan, I., Roife, M., Ruiz, S., Savary, G., Scherer, S.,
Scott, G., Shen, H., Shoshitelli, N., Sison, I., Sodergren, E.,
Sonnaike, T., Sparks, A., Stanbury, H., Stone, H., Sutton, A., Svarak, A.,
Taber, P., Tameria, K., Tameria, K., Tang, H., Tansey, J., Taylor, C.,
Taylor, T., Teifrod, B., Thomas, N., Thomas, S., Uman, K., Vasquez, L.,
Vera, V., Villalón, D., Vanson, R., Wang, Q., Wang, S., Ward-Moore, S.,
Warren, R., Washington, C., Watlington, S., Williams, G.,
Williamson, A., Wiczcyk, R., Woodson, S., Worley, K., Wu, C., Wu, Y.,
Wu, Y.F., Zhou, J., Zorrilla, S., Zorrilla, S., Zorrilla, S., Zorrilla, S.,
Gibbs, R.
Direct Submission
Unpublished
2 (bases 1 to 75555)
Worley, K.C.
Direct Submission
Submitted (12-JAN-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 75555)
Worley, K.C.
Direct Submission
Submitted (14-JUN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 75555)
Worley, K.C.
Direct Submission
Submitted (29-JUN-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 29, 2002 this sequence version replaced gi:21747431.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email
gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the
entire length of this clone. Overlapping regions of clones are only
sequenced and submitted once, so the sequence for the remainder of
the insert may be found in the record for the adjacent clones.
Overlapping clones are noted at the beginning and end of the
Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green,
unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
EST and cDNA sequences. Genes demonstrate at least two exons
flanked by consensus splice sites that maintained sequence
continuity across the splice junctions. Sequences that are not
identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
standard of double strand coverage with a minimum of 2 clones and 2
reads with no ambiguities or 2 chemistries with a minimum of 2
clones and 3 reads with no ambiguities. If the sequence quality for
a region does not meet this standard, it will be indicated in the
annotation as low coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
standards - estimated error rate less than 1 per 10,000 bases.
Reports of lowest quality individual bases and measures of base
quality are listed below. Description of the metrics can be found
at URL:
<http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

FEATURES

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Query Match 10.3%; Score 89; DB 9; Length 7555;
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DB 13063 GGGGTTTCAACGGTTAGCAGAGAGCTTCGAACTCTGATCGGCCGCT 13004
QY 96 CGGCTCCCAAGTGTGGATTACAGC 124
DB 13003 CGGCTCCCAAGTGTGGATTACAGC 12975

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RESULT 10
AC004537 88872 bp DNA linear PRI 08-OCT-2003
LOCUS Homo sapiens PAC clone RP5-872P7 from 7, complete sequence.
AC004537
AC004537
AC004537.1 GI:3041854
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 88872)
Sulston, J. B. and Wilson, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99063792
PUBMED
8847074
REFERENCE
1 (bases 1 to 88872)
Burkhart, J., Dauphin, S. and Elliott, G.
The sequence of Homo sapiens PAC clone RP5-872P7
Unpublished (2001)
3 (bases 1 to 88872)
Waterson, R.
Direct Submission
Submitted (09-APR-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
4 (bases 1 to 88872)
Waterson, R.
Direct Submission
Submitted (03-FEB-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
5 (bases 1 to 88872)
Wilson, R.
Direct Submission
Submitted (08-OCT-2003) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT
-----
Genome Center
Center: Washington University Genome Sequencing Center
Center code: MUGSC
Web site: http://genome.wustl.edu
Contact: saplen@wustl.wustl.edu
-----
Summary Statistics
Center project name: F_DV0872P07

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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/GTB/CHR7>, send <mailto:segreen@nhgri.nih.gov>, or see <http://genome.wustl.edu>

SOURCE INFORMATION:
This clone was derived from human PAC library RPCT-4, prepared by Pieter de Jong and coworkers at <http://www.Chori.org> using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor. The clone may be obtained either from Genome Systems, Inc. (<http://www.genomesystems.com>) or Research Genetics, Inc. (<http://www.resgen.com>); or from Pieter de Jong. VECTOR: pCYPAC2

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RPS-1100P23, 200 bp overlap. Actual start of this clone is at base position 111440 of RPS-1100P23 actual end is at 88872 of RPS-872F7.

FEATURES

Source
1. 88872
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/db_xref="taxon:9606"
/chromosome="7"
/map="7"
/clone="RPS-872F7"
/clone_id="RPCT-4"
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/rpt_family="Alu"
repeat_region
2125. 2155
/rpt_family="(TG)n"
4730. 4827
/rpt_family="L1"
5487. 6038
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6013. 6188
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6189. 6486
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6676. 6991
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7760. 8206
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8973. 9747
repeat_region

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9751. 9789
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9856. 10618
repeat_region
1130. 1164
/rpt_family="ERV1"
13378. 13589
/rpt_family="AT-rich"
13582. 13608
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16428. 16709
/rpt_family="ERV1"
16710. 17023
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17376. 17684
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17924. 18068
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18239. 18307
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18993. 19345
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19373. 19528
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19535. 19671
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19673. 19961
/rpt_family="MER2_type"
19963. 20504
/rpt_family="L2"
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21861. 21888
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26354. 26678
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27200. 27732
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30494. 30671
/rpt_family="MIR"
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32176. 32374
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32375. 32435
/rpt_family="GA-rich"
repeat_region


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repeat_region 9307..9359
/rpc_family="MTR"
repeat_region 9378..9535
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repeat_region 11955..11997
/rpc_family="CR1"
misc_feature 12114..12226
/note="match to EST AM682247 (NID:G8044257)"
repeat_region 12291..12575
/rpc_family="Alu"
/rpc_family="Alu"
misc_feature 12298..12312
/note="match to EST BE511578 (NID:G11594876)"
misc_feature 12317..12368
/note="match to EST BG149317 (NID:G12661347)"
repeat_region 12577..12911
/rpc_family="Alu"
/rpc_family="Alu"
misc_feature 12747..13320
/note="match to EST AA211096 (NID:G1809818) zq89g01.s1"
misc_feature 13489..13917
/note="match to EST AA210922 (NID:G1809594) zq89g01.r1"
repeat_region 16636..16651
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repeat_region 16652..16966
/rpc_family="Alu"
/rpc_family="Alu"
repeat_region 16967..17022
/rpc_family="L2"
/rpc_family="L2"
repeat_region 18362..18664
/rpc_family="Alu"
/rpc_family="Alu"
misc_feature 18605..19093
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/rpc_family="ACCTG)n"
repeat_region 20071..20183
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/rpc_family="ACGAGA)n"
repeat_region 21010..21167
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/rpc_family="ACGAGA)n"
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/rpc_family="Alu"
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repeat_region 21395..21437
/rpc_family="ACCTG)n"
/rpc_family="ACCTG)n"
repeat_region 21459..21637
/rpc_family="ACGAGA)n"
/rpc_family="ACGAGA)n"
repeat_region 21653..21754
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/rpc_family="ACGAGA)n"
repeat_region 21781..22322
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/rpc_family="ACGAGA)n"
repeat_region 22359..22717
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/rpc_family="ACGAGA)n"
repeat_region 23315..23406
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repeat_region 24007..24310
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/rpc_family="Alu"
repeat_region 25412..25605
/rpc_family="MIR"
/rpc_family="MIR"
repeat_region 26559..26865
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/rpc_family="Alu"
repeat_region 26882..27183
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repeat_region 27185..27246
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/rpc_family="MIR"
repeat_region 27247..27548
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/rpc_family="Alu"
repeat_region 27549..27567
/rpc_family="MIR"
/rpc_family="MIR"
repeat_region 27568..27855
/rpc_family="Alu"
/rpc_family="Alu"
repeat_region 27856..27882
/rpc_family="MIR"
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Query Match 10.3%, Score 89; DB 9; Length 149397;
Best Local Similarity 100.0%; Pred. No. 1.3e-40;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 GGGGTTTCACCGTGTGACGAGATGGTCTGAACTCTGACCTGATCGCCCGCT 95
Db 111428 GGGGTTTCACCGTGTGACGAGATGGTCTGAACTCTGACCTGATCGCCCGCT 111487
Qy 96 GGGGCTCCCAAGTGTGGATGACGAC 124
Db 111488 GGGGCTCCCAAGTGTGGATGACGAC 111516

RESULT 12
AC020890 152005 bp DNA linear PRI 15-MAR-2003
LOCUS BAC Library complete sequence.
DEFINITION Homo sapiens 3 BAC Rpl1-791s (Roswell Park Cancer Institute Human
AC020890
VERSION AC020890.22 GI:21553158
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 152005)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
Albrooks, S.L., Amaralunga, H.C., Are, J.R., Ayale, M., Banks, T.,
Barbata, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D.,
Bouck, J., Bowie, S., Brieval, M., Brown, B., Brown, M., Bryant, N.P.,
Bunay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carroll, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhury, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Dabonne, S.R., David, R.,
David, M.L., Davis, C., Davy-Carroll, L., Dedrich, D.A.,
DeLaney, K.R., Delgado, O., Dem, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Eamhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Franz, P.,
Gabisi, A., Gao, D., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorelli, D.H., Guvera, W., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlik, P., Hawes, A., He, X.,
Hernandez, J., Hernandez, O., Hodgson, A., Hoques, M., Hollway, C.,
Hollins, B., Homel, F., Howard, S., Huber, J., Huylk, S., Hune, J.,
Jackson, L.B., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
Joudan, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korah, J.,
Kovar, C., Kratovic, J., Kuresh, A., Landry, N., Leal, B., Lewis, L.C.,
Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, Y., Liu, W.,
Loulseged, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R.,
Ma, J., Maheshwari, M., Mapua, P., Martin, J.R., Martindale, A.,
Martinez, E., Massey, E., Mawhney, B., McLeod, M.P., Meador, M.,
Mei, G., Metzker, M., Miner, Z., Miner, Z., Mitchell, T., Mohabbat, K.,
Moore, S., Morgan, M., Moorish, T., Morris, S., Moser, M., Neal, D.,
Nelson, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
Niederson, E., Nwokkwo, S., Ogutu, M., Okunju, G., Oragunye, N.,
Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, N.,
Plekens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rivers, M.,
Rojas, A., Rojokokan, I., Rolfe, M., Ruliz, S., Sany, G., Scherer, S.,
Scott, G., Shen, H., Shoshchani, N., Sisson, I., Sodergren, B.,
Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutcliffe, A., Svarek, A.,
Taber, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansley, J., Taylor, C.,
Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vazquez, L.,
Vera, V., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S.,
Warren, R., Washington, C., Watlington, S., Williams, G.,

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repeat_region      /rpt_family="LJM4"
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                    /rpt_family="(TTTTG)n"
repeat_region      complement(11728..12011)
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Query Match      10.3%; Score 89; DB 9; Length 152005;
Best Local Similarity 100.0%; Pred. No. 1.3e-40;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 74493 GGGGTTTACCGGTAGCCAGAGATGCTCGAAGCTCGTGAATCCGCGCCGCT 95
          GGGGTTTACCGGTAGCCAGAGATGCTCGAAGCTCGTGAATCCGCGCCGCT 74434
QY 96 CGGCTTCCCAAGTGTGGATTACAGGC 124
          CGGCTTCCCAAGTGTGGATTACAGGC 74405
Db 74433 CGGCTTCCCAAGTGTGGATTACAGGC 74405

RESULT 13
AL683875/c
LOCUS             184927 bp DNA linear HTG 02-APR-2003
DEFINITION        Homo sapiens chromosome X clone RP11-446K8, 5 unordered pieces.
ACCESSION         AL683875
VERSION           AL683875.25 GI:29498394
KEYWORDS          HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE            Homo sapiens
ORGANISM          Homo sapiens (human)
REFERENCE          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE             1 (bases 1 to 184927)
JOURNAL            Lawlor S.
COMMENT            Direct Submission
                    Submitted (02-APR-2003) Wellcome Trust Sanger Institute, Hinxton,
                    Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                    humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
                    On Apr 2, 2003 this sequence version replaced gi:28971596.
                    ----- Genome Center
                    Center: Wellcome Trust Sanger Institute
                    Center code: SC
                    Web site: http://www.sanger.ac.uk
                    Contact: humquerry@sanger.ac.uk
                    Project Information
                    -----
                    Center project name: h446K8
                    ----- Summary Statistics
                    Assembly program: XGAP4; version 4.5
                    Chemistry: Dye-terminator Big Dye; 13% of reads
                    Consensus quality: 182378 bases at least Q40
                    Consensus quality: 183253 bases at least Q30
                    Consensus quality: 183854 bases at least Q20
                    Insert size: 184527; sum-of-coverage
                    Insert size: 179006; 2.7% error; agarose-fp
                    Quality coverage: 9.16x in Q20 bases; sum-of-coverage quality
                    coverage: 10.59x in Q20 bases; agarose-fp

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* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 49340: contig of 49340 bp in length
* 49341 49440: gap of 100 bp
* 49441 91479: contig of 42039 bp in length
* 91480 91579: gap of 100 bp
* 91580 94862: contig of 3283 bp in length
* 94863 94962: gap of 100 bp
* 94963 119846: contig of 24884 bp in length
* 119847 119946: gap of 100 bp
* 119947 184927: contig of 64981 bp in length.

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FEATURES
source
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="X"
/clone_id="RP11-446K8"
/clone_id="RPCT-11.2"
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/note="assembly_fragment:04719
clone_end:77
vector_side:left"
49441..91479
/note="assembly_fragment:00421"
91580..94862
/note="assembly_fragment:01738"
94963..119846
/note="assembly_fragment:04642"
119947..184927
/note="assembly_fragment:04655
clone_end:56
vector_side:right"

ORIGIN
Query Match      10.3%; Score 89; DB 2; Length 184927;
Best Local Similarity 100.0%; Pred. No. 1.3e-40;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 169617 GGGGTTTACCGGTAGCCAGAGATGCTCGAAGCTCGTGAATCCGCGCCGCT 169618
          GGGGTTTACCGGTAGCCAGAGATGCTCGAAGCTCGTGAATCCGCGCCGCT 169589
QY 96 CGGCTTCCCAAGTGTGGATTACAGGC 124
          CGGCTTCCCAAGTGTGGATTACAGGC 169589
Db 169617 CGGCTTCCCAAGTGTGGATTACAGGC 169589

RESULT 14
AL683807/c
LOCUS             189825 bp DNA linear PRI 23-NOV-2002
DEFINITION        Human DNA sequence from clone RP13-297E16 on chromosome X, complete
sequence.
ACCESSION         AL683807
VERSION           AL683807.22 GI:25251452
KEYWORDS          HTG.
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
REFERENCE          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE             1 (bases 1 to 189825)
JOURNAL            Grahan, D.
COMMENT            Direct Submission
                    Submitted (22-NOV-2002) Wellcome Trust Sanger Institute, Hinxton,
                    Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                    humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
                    On Nov 24, 2002 this sequence version replaced gi:24474461.
                    ----- Genome Center
                    Center: Wellcome Trust Sanger Institute
                    Center code: SC
                    Web site: http://www.sanger.ac.uk
                    Contact: humquerry@sanger.ac.uk

```

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During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMBASE; Information
on the WORMBASE database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormmap This sequence

```

was generated from part of bacterial clone contigs of human chromosome X. Further information can be found at <http://www.sanger.ac.uk/HGP/ChrX>
 RP13-297E16 is from the library RPCI-13.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>
 VECTOR: pBAC3.6

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

FEATURES

source

location/Qualifiers
 1..189825
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="X"
 /clone_lib="RP13-297E16"
 /clone_lib="RPCI-13.2"

ORIGIN

Query Match 10.3%; Score 89; DB 9; Length 189825;
 Best Local Similarity 100.0%; Pred. No. 1.3e-40;
 Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 GGGGTTACCCGTTAGCAGATGCTCTGCACTCTGACCTCGATCCGCCCT 95
 |||||
 Db 88862 GGGGTTACCCGTTAGCAGATGCTCTGCACTCTGACCTCGATCCGCCCT 88803

QY 96 CGGCTCCCAAGTCTGATTAACAGC 124
 |||||
 Db 88802 CGGCTCCCAAGTCTGATTAACAGC 88774

RESULT 15
 AL355146 57447 bp DNA linear PRI 21-DEC-2000
 LOCUS Human DNA sequence from clone RP11-31101 on chromosome 6, complete
 DEFINITION
 accession AL355146
 version AL355146.13 GI:11967512
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 57447)
 TRACEY, A.
 Direct Submission
 Submitted (19-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: hunquerry@sanger.ac.uk
 requests: clonerequests@sanger.ac.uk
 On Dec 22, 2000 this sequence version replaced gi:11876034.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.

This sequence has been finished according to sequence map criteria
 as follows. An attempt is made to resolve all sequencing problems,
 such as compressions and repeats, but not necessarily within known
 annotated repeat sequence elements. Where the sequence is
 ambiguous, there is an annotation using the 'unsure' feature key.
 The following abbreviations are used to associate primary accessions
 numbers given in the feature table with their source databases:
 Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
 on the WORMPEP database can be found at

FEATURES

source

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
 was generated from part of bacterial clone contigs of human
 chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
 Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr6>
 RP11-31101 is from the library RPCI-11.2 constructed by the group
 of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
 VECTOR: pBAC3.6
 IMPORTANT: This sequence is not the entire insert of clone
 RP11-31101. It may be shorter because we sequence overlapping
 sections only once, except for a 100 base overlap.
 The true left end of clone RP11-31101 is at 1 in this sequence. The
 true left end of clone RP11-135M8 is at 57348 in this sequence.

location/Qualifiers
 1..57447
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /chromosome="6"
 /clone_lib="RP11-31101"
 /clone_lib="RPCI-11.2"
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 /note="LIM2 repeat: matches -668..-492 of consensus"
 1516..1540
 /note="MER31 repeat: matches 100..124 of consensus"
 1835..2687
 /note="L1 repeat: matches 3631..4476 of consensus"
 2664..2937
 /note="L1M1 repeat: matches 5517..5793 of consensus"
 2938..2965
 /note="L1 copies 2 mer ca 100% conserved"
 2967..3380
 /note="L1P1A6 repeat: matches 5783..6149 of consensus"
 complement(3594..4086)
 /note="match: GSS: Em:AQ451181"
 3898..4140
 /note="L2 repeat: matches 2492..2750 of consensus"
 complement(4026..4542)
 /note="match: GSS: Em:AQ720695"
 4247..4545
 /note="L1A81 repeat: matches 7..302 of consensus"
 4871..5162
 /note="L1A59 repeat: matches 1..292 of consensus"
 5207..5253
 /note="L1M46 repeat: matches 5151..6299 of consensus"
 5563..6744
 /note="L1M82 repeat: matches 5812..6002 of consensus"
 6774..7192
 /note="L1M2 repeat: matches 5312..5763 of consensus"
 7227..7497
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 7505..7628
 /note="L1M46 repeat: matches 6141..6265 of consensus"
 7647..7963
 /note="L1M4 repeat: matches 2670..3000 of consensus"
 8755..8938
 /note="L1R repeat: matches 58..245 of consensus"
 9625..9854
 /note="L1R repeat: matches 24..262 of consensus"
 12052..12222
 /note="L1R repeat: matches 360..533 of consensus"
 14872..14936
 /note="L1R repeat: matches 232..293 of consensus"
 complement(15388..15883)
 /note="match: GSS: Em:AQ719416"
 15566..15613
 /note="L2 copies 2 mer ca 72% conserved"
 18406..24551
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 24575..24903
 /note="MER58B repeat: matches 1..341 of consensus"
 27188..27305
 repeat_region

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repeat_region /note="MIR repeat: matches 81. .205 of consensus"
27440. .27491
/note="L2 repeat: matches 2639. .2690 of consensus"
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/note="L2 repeat: matches 2432. .2534 of consensus"
28606. .28672
/note="ORSL repeat: matches 238. .302 of consensus"
28701. .28874
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repeat_region 28703. .28786
/note="AluJo/FRAM repeat: matches 199. .262 of consensus"
28711. .28916
/note="match: GSS: Em:AQ615327"
misc_feature complement(28771. .28966)
/note="match: GSS: Em:A2385385"
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/note="40 copies 2 mer at 76% conserved"
29064. .29313
/note="L1M4 repeat: matches 4738. .4986 of consensus"
29314. .29607
/note="AluSx repeat: matches 1. .306 of consensus"
29608. .30913
/note="L1M4 repeat: matches 4986. .6300 of consensus"
30946. .31112
/note="L1M6 repeat: matches 5938. .6108 of consensus"
complement(31361. .31864)
/note="match: GSS: Em:AQ120459"
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33925. .34161
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34211. .34306
/note="MIR repeat: matches 48. .146 of consensus"
35045. .35108
/note="L1M3 repeat: matches 5891. .5951 of consensus"
35119. .35267
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35268. .35513
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35593. .35780
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36952. .37065
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43305. .43385
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43386. .44026
/note="L1P16 repeat: matches 5509. .6157 of consensus"
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44378. .44457
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44718. .44985
/note="L2 repeat: matches 2005. .2286 of consensus"
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/note="match: GSS: Em:AQ059083"
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49133. .49340
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49999. .50436
/note="L1M4 repeat: matches 6655. .7093 of consensus"

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/note="AluSx repeat: matches 1. .312 of consensus"
repeat_region 51887. .52533
/note="L2 repeat: matches 1434. .2116 of consensus"
52544. .52819
/note="MT2A repeat: matches 174. .453 of consensus"
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/note="L2 repeat: matches 2579. .2678 of consensus"
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/note="THERC repeat: matches 291. .369 of consensus"
55720. .56032
/note="AluSx repeat: matches 1. .306 of consensus"
56033. .56348
/note="THERC repeat: matches 7. .291 of consensus"
56955. .57266
/note="AluSx repeat: matches 1. .302 of consensus"
complement(57062. .57330)
/note="match: GSS: Em:AQ487215"
misc_feature

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DB 35420 GTTACCGTGTACCGAGATGCTGAACTCTGACCTGATCCGCCCTCGG 35479
QY 99 CTTCCAAAGTCTGGAGTTACAGGC 124
DB 35480 CTTCCAAAGTCTGGAGTTACAGGC 35505

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Search completed: May 24, 2004, 17:39:20
Job time : 2505 secs

PR 19-AUG-1997; 97US-0056563P.
 PR 19-AUG-1997; 97US-0056731P.
 PR 19-AUG-1997; 97US-0056732P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Soppet DR, Edner R, Olsen HS, Young PE, Greene JM;
 PI Ferrie AM, Yu G, Ni J, Rosen CA, Brewer LA, Janat F;
 XX
 DR WPI: 1999-167452/14.
 DR P-RSDB; AAT10846.
 PT
 PT New isolated human genes encoding secreted polypeptides - useful for
 PT diagnosis and treatment of pathological diseases.
 XX
 PS Claim 3; Page 253-254; 331pp; English.
 CC The specification describes secreted proteins and their corresponding
 CC polynucleotides which are useful for preventing, treating or ameliorating
 CC medical conditions, e.g. by protein or gene therapy. Pathological
 CC conditions can also be diagnosed by determining the amount of the
 CC secreted polypeptides in a sample or by determining the presence of
 CC mutations in the polynucleotides. Specific uses are described for each of
 CC the products, based on which tissues they are most highly expressed in,
 CC and include developing products for the diagnosis or treatment of cancer,
 CC tumours, neurodegenerative disorders, developmental abnormalities and
 CC foetal deficiencies, blood disorders, CNS disorders, diseases of the
 CC immune system, autoimmune diseases, hepatic and renal disease, diabetes,
 CC inflammation, allergies, ischemic shock, Alzheimer's and cognitive
 CC disorders, schizophrenia, cardiovascular disorders, prostate diseases,
 CC asthma, disorders involving osteoclasts such as osteoporosis, arthritis
 CC or malignancies, diseases of testes, lung or thymus, digestive/endocrine
 CC disorders, infections and AIDS. The polypeptides are also useful for
 CC identifying their binding partners
 CC
 SQ Sequence 867 BP; 219 A; 231 C; 222 G; 192 T; 0 U; 3 Other;
 Query Match 100.0%; Score 867; DB 2; Length 867;
 Best Local Similarity 100.0%; Pred. No. 5.4e-308;
 Matches 867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 721 CAGGCGCGAGCTGGGACAGAGCAGATCCGCAAGAGGCTGTGAGCAGCTCTGGAGCCAA 780
 DB 721 CAGGCGCGAGCTGGGACAGAGCAGATCCGCAAGAGGCTGTGAGCAGCTCTGGAGCCAA 780
 QY 781 GCACTCGGATTTGAACCCCGGCTCTTCAAGCTCAAGCTGTGTACCTTGATGAAYCAC 840
 DB 781 GCACTCGGATTTGAACCCCGGCTCTTCAAGCTCAAGCTGTGTACCTTGATGAAYCAC 840
 QY 841 TGCTATGACCAATCTCGTCCGCAATTC 867
 DB 841 TGCTATGACCAATCTCGTCCGCAATTC 867
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 ID ADB47729 standard; cDNA; 867 BP.
 XX
 AC ADB47729;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE
 DE Novel human secreted protein cDNA #2.
 XX
 KW ss; gene; human; secreted protein; insulin; haemoglobin S; haemoglobin B;
 KW superoxide; SOD; catalase; DNA repair protein; oncogene;
 KW tumour suppressor; tumour necrosis factor; TNF; inflammation;
 KW blood vessel growth inhibition; immune response; immune system disorder;
 KW hyperproliferative disorder; neoplasm; cardiovascular disorder;
 KW peripheral artery disease; limb ischemia; arterio-arterial fistula;
 KW arteriovenous fistula; congenital heart defect;
 KW neovascularisation disorder; wound healing;
 KW epithelial cell proliferation; neurological disease; Alzheimer's disease;
 KW Parkinson's disease; Huntington's disease; mania; dementia;
 KW infectious disease.
 XX
 OS Homo sapiens.
 XX
 PN US2003054443-A1.
 XX
 PD 20-MAR-2003.
 XX
 PF 04-OCT-2001; 2001US-00969730.
 XX
 PR 05-AUG-1997; 97US-0054798P.
 PR 05-AUG-1997; 97US-0054803P.
 PR 05-AUG-1997; 97US-0054804P.
 PR 05-AUG-1997; 97US-0054806P.
 PR 05-AUG-1997; 97US-0054807P.
 PR 05-AUG-1997; 97US-0054808P.
 PR 05-AUG-1997; 97US-0054809P.
 PR 05-AUG-1997; 97US-0055310P.
 PR 05-AUG-1997; 97US-0055311P.
 PR 05-AUG-1997; 97US-0055312P.
 PR 05-AUG-1997; 97US-0055386P.
 PR 18-AUG-1997; 97US-0055970P.
 PR 18-AUG-1997; 97US-0055986P.

PR 19-AUG-1997; 57US-0056364P.
PR 19-AUG-1997; 57US-0056365P.
PR 19-AUG-1997; 57US-0056366P.
PR 19-AUG-1997; 57US-0056367P.
PR 19-AUG-1997; 57US-0056370P.
PR 19-AUG-1997; 57US-0056371P.
PR 19-AUG-1997; 57US-0056557P.
PR 19-AUG-1997; 57US-0056563P.
PR 19-AUG-1997; 57US-0056731P.
PR 19-AUG-1997; 57US-0056732P.
PR 04-AUG-1998; 58WC-US016235.
PR 04-FEB-1999; 99US-00244112.
PR 06-OCT-2000; 2000US-0238291P.
PR 01-FEB-2001; 2001US-00774639.
XX
XX (RUBE/) RUBEN S. M.
PA (SOPP/) SOPPET D. R.
PA (BENE/) BENER R.
PA (OLSE/) OLSEN H. S.
PA (YOUN/) YOUNG P. E.
PA (GREEN/) GREENE J. M.
PA (FERR/) FERRIE A. M.
PA (YUGG/) YUG G.
PA (NITU/) NI J.
PA (ROSE/) ROSEN C. A.
PA (BREM/) BREWER I. A.
PA (JANA/) JANAT F.
PA (BIRS/) BIRSE C. E.
PI Ruben SM, Soppet DR, Ebner R, Olsen HS, Young PE, Greene JM;
PI Ferrie AM, Yu G, Ni J, Rosen CA, Brewer IA, Janet F, Birse CE;
XX WPI: 2003-695903/66.
XX P-PSDB; ADB47826.
XX
XX Novel human secreted proteins useful for treating and/or diagnosing
PT disorders of immune system, cardiovascular disorders such as peripheral
PT artery disease, neurological diseases such as Alzheimer's disease.
XX
XX
XX Claim 3; Page 205; 333pp; English.
XX
XX The invention relates to novel human secreted proteins. The protein is
CC useful for preventing, treating or ameliorating a medical condition. The
CC protein is useful for diagnosing a pathological condition or
CC susceptibility to a pathological condition in a subject. The protein is
CC useful for identifying a binding partner. The nucleic acid is useful for
CC diagnosing pathological condition or a susceptibility to pathological
CC condition in a subject. The protein is useful as reagents for
CC differential identification of the tissues or cell types present in a
CC biological sample. The protein can be administered to patients having
CC absent or decreased levels of polypeptides e.g. insulin, to supplement
CC absent or decreased levels of different polypeptides, e.g. haemoglobin S
CC for haemoglobin B, superoxidease (SOD), catalase, DNA repair protein, to
CC inhibit the activity of a polypeptide e.g. an oncogene or tumour
CC suppressor, to activate the activity of polypeptide e.g. by binding to a
CC receptor, to reduce the activity of membrane bound receptor by competing
CC with it for free ligand e.g. soluble tumour necrosis factor (TNF)
CC receptors used in reducing inflammation, or to bring about a desired
CC response e.g. blood vessel growth inhibition, enhancement of immune
CC response to proliferative cells or tissues. The protein and the nucleic
CC acid are useful for treating, preventing, detecting, diagnosing disorder
CC of immune system involving abnormal growth of specific types of cells as
CC well as of other cell types where expression has been observed. The
CC protein, the nucleic acid and antibodies are useful for treating,
CC preventing and/or diagnosing diseases, disorders and/or conditions of
CC immune system, hyperproliferative disorders including neoplasms,
CC cardiovascular disorders (such as peripheral artery disease, limb
CC ischaemia, arterio-arterial fistula, arteriovenous fistula, congenital
CC heart defects, etc), neovascularisation disorders, wound healing and
CC epithelial cell proliferation, neurological diseases (such as Alzheimer's
CC disease, Parkinson's disease, Huntington's disease, mania, dementia,
CC etc), infectious diseases caused by virus, bacteria, fungi, etc. The
CC present sequence represents a cDNA encoding a novel human secreted

CC	protein.
XX	
SQ	Sequence 867 BP; 219 A; 231 C; 222 G; 192 T; 0 U; 3 Other;
	Query Match 100.0%; Score 867; DB 9; Length 867; Best Local Similarity 100.0%; Pred. No. 5,4e-308; Matches 867; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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OY	781 GCCACTCGGATTTGAACCCCAGGCTCTCTCAAGSTCAGCTGTGTGAGCCTTGANTGAAYCAC 840
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ID	ABZ68140/C
XX	ABZ68140 standard; DNA; 58181 BP.

DR WPI: 2002-188264/24.
XX Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX
PS Claim 1; SEQ ID NO 7550; 44pp; English.
XX
CC The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABU61664
CC to ABU70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms
CC tumour
XX
SQ Sequence 145831 BP; 37379 A; 35440 C; 35158 G; 37854 T; 0 U; 0 Other;
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Query Match 11.3%; Score 98; DB 6; Length 145831;
Best Local Similarity 100.0%; Pred. No. 5.1e-27;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 27 AGTAGAGATGGGGTTTACCGGTGTACCGAGATGCTCGAAGCTCCTGACCTCGATG 86
DB 36600 AGTAGAGATGGGGTTTACCGGTGTACCGAGATGCTCGAAGCTCCTGACCTCGATG 86541
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DB 38540 CGCCCGCGCTCGGCTCCCAAGTCTGGATTACAGGC 38503
XX
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ID ABL66806 standard; DNA; 145831 BP.
XX
XX ABL66806;
XX
XX
XX 15-MAY-2002 (first entry)
XX
XX
XX Lung cancer related gene sequence SEQ ID NO:5143.
XX
XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
XX stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
XX cytostatic; gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;
XX gene; ds.
XX
XX Homo sapiens.
XX
XX WO200194629-A2.
XX
XX 13-DEC-2001.
XX
XX
XX 30-MAY-2001; 2001MO-US010838.
XX
XX
XX 05-JUN-2000; 2000US-0209473P.
XX
XX 05-JUN-2000; 2000US-0209531P.
XX
XX 18-SEP-2000; 2000US-0231333P.
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XX 18-SEP-2000; 2000US-0233617P.
XX
XX 20-SEP-2000; 2000US-0234009P.
XX
XX 20-SEP-2000; 2000US-0234034P.
XX
XX 20-SEP-2000; 2000US-0234052P.
XX
XX 22-SEP-2000; 2000US-0234509P.
XX
XX 22-SEP-2000; 2000US-0234567P.
XX

PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 25-SEP-2000; 2000US-0235377P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX
XX (AVAL-) AVALON PHARM.
XX
XX Young PR, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
XX Soppet DR, Weaver Z;
XX
XX WPI: 2002-188264/24.
XX
XX
XX Screening for anti-neoplastic agent involves exposing cells to a chemical
XX agent to be tested for anti-neoplastic activity, and determining a change
XX in expression of a gene of a signature gene set.
XX
XX
XX Claim 1; SEQ ID NO 5143; 44pp; English.
XX
XX
XX The present invention describes a method (M1) for screening for an anti-
XX neoplastic agent. The method involves exposing cells to a chemical agent
XX to be tested for anti-neoplastic activity, determining a change in
XX expression of at least one gene (I) of a signature gene set, where (I)
XX comprises a sequence (S) selected from 8447 sequences (given in ABU61664
XX to ABU70110), or is at least 95% identical to (S), where a change in
XX expression is indicative of anti-neoplastic activity. (I) has cytostatic
XX activity and can be used in gene therapy. M1 can be used for screening an
XX anti-neoplastic agent, and can be used for producing a product which is
XX the data collected with respect to the anti-neoplastic agent as a result
XX of M1, and the data is sufficient to convey the chemical structure and/or
XX properties of the agent. M1 can be used in the treatment of cancer such
XX as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
XX prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
XX cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
XX cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms'
XX tumour
XX
XX
XX Sequence 145831 BP; 37379 A; 35440 C; 35158 G; 37854 T; 0 U; 0 Other;
XX
XX
XX Query Match 11.3%; Score 98; DB 6; Length 145831;
XX Best Local Similarity 100.0%; Pred. No. 5.1e-27;
XX Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX
XX 27 AGTAGAGATGGGGTTTACCGGTGTACCGAGATGCTCGAAGCTCCTGACCTCGATG 86
XX
XX
XX

DB 38600 AGTAGAGATGGGGTTTCACCGTGTAGCCAGGATGGCTGCAACTCTGACTGCTGATC 38541

QY 87 CGCCCGCCTCGGCTCCCAAGTGTGGATTACAGGC 124

DB 38540 CGCCCGCCTCGGCTCCCAAGTGTGGATTACAGGC 38503

RESULT 8

ABL6858/c

ID ABL68588 standard; DNA; 145831 BP.

XX ABL68588;

AC

XX 15-MAY-2002 (first entry)

DT

XX Kidney cancer related gene sequence SEQ ID NO:6925.

DE

XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;

KM stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;

KM cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;

KM gene; ds.

XX Homo sapiens.

OS

XX WO200194629-A2.

PN

XX 13-DEC-2001.

PD

XX 30-MAY-2001; 2001WO-US010838.

PF

XX

XX 05-JUN-2000; 2000US-0209473P.

PR 05-JUN-2000; 2000US-0209531P.

PR 18-SEP-2000; 2000US-0233133P.

PR 18-SEP-2000; 2000US-0233617P.

PR 20-SEP-2000; 2000US-0234009P.

PR 20-SEP-2000; 2000US-0234034P.

PR 20-SEP-2000; 2000US-0234052P.

PR 22-SEP-2000; 2000US-0234509P.

PR 22-SEP-2000; 2000US-0234567P.

PR 25-SEP-2000; 2000US-0234923P.

PR 25-SEP-2000; 2000US-0234924P.

PR 25-SEP-2000; 2000US-0235077P.

PR 25-SEP-2000; 2000US-0235082P.

PR 25-SEP-2000; 2000US-0235134P.

PR 25-SEP-2000; 2000US-0235280P.

PR 26-SEP-2000; 2000US-0235637P.

PR 26-SEP-2000; 2000US-0235638P.

PR 27-SEP-2000; 2000US-0235711P.

PR 27-SEP-2000; 2000US-0235720P.

PR 27-SEP-2000; 2000US-0235840P.

PR 27-SEP-2000; 2000US-0235863P.

PR 28-SEP-2000; 2000US-0236028P.

PR 28-SEP-2000; 2000US-0236032P.

PR 28-SEP-2000; 2000US-0236033P.

PR 28-SEP-2000; 2000US-0236034P.

PR 28-SEP-2000; 2000US-0236109P.

PR 28-SEP-2000; 2000US-0236111P.

PR 29-SEP-2000; 2000US-0236842P.

PR 29-SEP-2000; 2000US-0236891P.

PR 02-OCT-2000; 2000US-0237172P.

PR 02-OCT-2000; 2000US-0237173P.

PR 02-OCT-2000; 2000US-0237278P.

PR 02-OCT-2000; 2000US-0237294P.

PR 02-OCT-2000; 2000US-0237295P.

PR 02-OCT-2000; 2000US-0237316P.

PR 03-OCT-2000; 2000US-0237425P.

PR 03-OCT-2000; 2000US-0237598P.

PR 03-OCT-2000; 2000US-0237604P.

PR 03-OCT-2000; 2000US-0237606P.

PR 03-OCT-2000; 2000US-0237608P.

PR 01-NOV-2000; 2000US-0241867P.

PR 01-NOV-2000; 2000US-0245084P.

XX

PA (AVALON PHARM.

XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;

PI Soppet DR, Weaver Z;

PI

XX WPI; 2002-188264/24.

DR

XX Screening for anti-neoplastic agent involves exposing cells to a chemical

PT agent to be tested for anti-neoplastic activity, and determining a change

PT in expression of a gene of a signature gene set.

XX

XX Claim 1; SEQ ID NO 6925; 44pp: English.

PS

XX The present invention describes a method (M1) for screening for an anti-

CC neoplastic agent. The method involves exposing cells to a chemical agent

CC to be tested for anti-neoplastic activity, determining a change in

CC expression of at least one gene (I) of a signature gene set, where (I)

CC comprises a sequence (S) selected from 847 sequences (given in ABL61664

CC to ABL70110), or is at least 95% identical to (S), where a change in

CC expression is indicative of anti-neoplastic activity. (I) has cytostatic

CC activity and can be used in gene therapy. M1 can be used for screening an

CC anti-neoplastic agent, and can be used for producing a product which is

CC the data collected with respect to the anti-neoplastic agent as a result

CC of M1, and the data is sufficient to convey the chemical structure and/or

CC properties of the agent. M1 can be used in the treatment of cancer such

CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,

CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell

CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous

CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's

CC tumour

XX

XX Sequence 145831 BP; 37379 A; 35440 C; 35158 G; 37854 T; 0 U; 0 Other;

SO

QY 27 AGTAGAGATGGGGTTTCACCGTGTAGCCAGGATGGCTGCAACTCTGACTGCTGATC 86

DB 38600 AGTAGAGATGGGGTTTCACCGTGTAGCCAGGATGGCTGCAACTCTGACTGCTGATC 38541

QY 87 CGCCCGCCTCGGCTCCCAAGTGTGGATTACAGGC 124

DB 38540 CGCCCGCCTCGGCTCCCAAGTGTGGATTACAGGC 38503

RESULT 9

ABL62309/c

ID ABL62309 standard; DNA; 145831 BP.

XX

XX ABL62309;

AC

XX 15-MAY-2002 (first entry)

DT

XX Colon adenocarcinoma related gene sequence SEQ ID NO:646.

DE

XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;

KM stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;

KM cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;

KM gene; ds.

XX Homo sapiens.

OS

XX WO200194629-A2.

PN

XX 13-DEC-2001.

PD

XX 30-MAY-2001; 2001WO-US010838.

PF

XX 05-JUN-2000; 2000US-0209473P.

PR 05-JUN-2000; 2000US-0209531P.

PR 18-SEP-2000; 2000US-0233133P.

PR 18-SEP-2000; 2000US-0233617P.

XX

Db 38600 AGTAGGATGGGCTTACCGGTGTAGCCAGATGCTCTGAACTCTGACCTCTGTGATC 38541
OY 87 CCGCGCGCTCGGCTCTCCAAAGTGTGGATTACAGGC 124
Db 38540 CCGCGCGCTCGGCTCTCCAAAGTGTGGATTACAGGC 38503

RESULT 11
AAK82012
ID AAK82012 standard; DNA; 49561 BP.
XX
AC AAK82012;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36824.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001MO-US001354.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205155P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214866P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 14-AUG-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225457P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226686P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0228927P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.

PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231966P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0235464P.
PR 26-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235835P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239933P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240950P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246533P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.

PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249298P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-483426/52.
 XX
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and metastasis.
 XX
 PS Disclosure; SEQ ID NO 36824; 3071pp + Sequence Listing; English.

CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting the
 CC nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
 CC represent sequences used in the exemplification of the present invention
 XX
 XX Sequence 49561 BP; 14811 A; 9800 C; 9812 G; 15138 T; 0 U; 0 Other;

Query Match 9.9%; Score 86; DB 4; Length 49561;
 Best Local Similarity 100.0%; Pred. No. 1.6e-22;
 Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 GGCGTTTACCGGTGTTAGCCAGGATGCTCGAAGCTCTGACTCGTGAATCCGCCCT 95
 DB 13127 GGCGTTTACCGGTGTTAGCCAGGATGCTCGAAGCTCTGACTCGTGAATCCGCCCT 13186
 QY 96 GGCGTTTACCGGTGTTAGCCAGGATGCTCGAAGCTCTGACTCGTGAATCCGCCCT 121
 DB 13187 GGCGTTTACCGGTGTTAGCCAGGATGCTCGAAGCTCTGACTCGTGAATCCGCCCT 13212

RESULT 12
 AAI62868
 ID AAI62868 standard; DNA; 267 BP.
 XX
 AC AAI62868;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human genomic DNA SEQ ID NO 196.
 XX

KM Human; nootropic; neuroprotective; cytoskeletal; dermatological; virucide;
 KM immunosuppressive; anti-inflammatory; anti-HIV; antibacterial; antiviral;
 KM antiparkinsonian; antispasmodic; antianemic; antidiabetic; cancer;
 KM antihemetic; hepatoprotective; cerebroprotective; antiinflammatory;
 KM antiallergic; antidiabetic; antileukemic; anticonvulsant; antifungal;
 KM antiparasitic; cardiac; immune disorder; cardiovascular disorder;
 KM neurological disease; infection; nephrotoxic; gene therapy; vaccine; ds.
 OS Homo sapiens.
 XX
 XX WO200155449-A1.
 XX
 XX 02-AUG-2001.
 XX
 XX 17-JAN-2001; 2001US-0001346.
 XX
 XX 31-JAN-2000; 2000US-0179065P.
 XX 04-FEB-2000; 2000US-0180628P.
 XX 19-MAY-2000; 2000US-0205151P.
 XX 07-JUL-2000; 2000US-0216880P.
 XX 14-JUL-2000; 2000US-0218290P.
 XX 14-AUG-2000; 2000US-0225447P.
 XX 01-SEP-2000; 2000US-0225443P.
 XX 06-SEP-2000; 2000US-0230437P.
 XX 08-SEP-2000; 2000US-0231243P.
 XX 25-SEP-2000; 2000US-0234997P.
 XX 29-SEP-2000; 2000US-0236367P.
 XX 13-OCT-2000; 2000US-0239937P.
 XX 08-NOV-2000; 2000US-0244676P.
 XX 08-NOV-2000; 2000US-0246477P.
 XX 08-NOV-2000; 2000US-0246525P.
 XX 08-NOV-2000; 2000US-0246526P.
 XX 08-NOV-2000; 2000US-0246528P.
 XX 17-NOV-2000; 2000US-0249210P.
 XX 17-NOV-2000; 2000US-0249211P.
 XX 17-NOV-2000; 2000US-0249214P.
 XX 17-NOV-2000; 2000US-0249215P.
 XX 01-DEC-2000; 2000US-0250160P.
 XX 01-DEC-2000; 2000US-0250391P.
 XX 05-DEC-2000; 2000US-0251030P.
 XX 05-DEC-2000; 2000US-0251988P.
 XX 05-DEC-2000; 2000US-0256719P.
 XX 06-DEC-2000; 2000US-0251479P.
 XX 08-DEC-2000; 2000US-0251989P.
 XX 08-DEC-2000; 2000US-0251990P.
 XX 11-DEC-2000; 2000US-0254097P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Barash SC, Ruben SM;
 XX WPI; 2001-476225/51.
 XX
 PT Novel plasma membrane associated proteins useful for diagnosing,
 PT treating, preventing and/or prognosing disorders related to the proteins,
 PT including cancer, immune response and neuronal disorders.
 XX
 PS Example 2; SEQ ID NO 196; 532pp + Sequence Listing; English.

The invention relates to novel genes (AAI62752-AAI62961) and proteins (AAI42347-AAI42415) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic

CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at http://wipo.int/publ/published_pct_sequences

XX Sequence 267 BP; 42 A; 93 C; 72 G; 60 T; 0 U; 0 Other;

Query Match 8.7%; Score 75; DB 4; Length 267;
 Best Local Similarity 100.0%; Pred. No. 4.7e-18;

Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 193 CTTCTGACCTCGATGCGCGCGCTCGGCTCCCAAGGCTGAGATTACAGGCATGAG 129

DB 193 CTTCTGACCTCGATGCGCGCGCTCGGCTCCCAAGGCTGAGATTACAGGCATGAG 252

QY 130 CCACTGCGCCAGCC 144

DB 253 CCACTGCGCCAGCC 267

RESULT 13
 AAH09234
 ID AAH09234 standard; cDNA; 579 BP.

AC AAH09234;

DT 26-JUN-2001 (first entry)

DE Human cDNA clone (3'-primer) SEQ ID NO:6069.

KM Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

OS Homo sapiens.

PN EP1074617-A2.

PD 07-FEB-2001.

PF 28-JUL-2000; 2000EP-00116126.

PR 28-JUL-1999; 99JP-00248036.

PR 27-AUG-1999; 99JP-00300253.

PR 11-JAN-2000; 2000JP-00118776.

PR 02-MAY-2000; 2000JP-00183767.

PR 09-JUN-2000; 2000JP-00241899.

PA (HELI-) HELIX RES INST.

PI Ota T, Isegai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

DR WPI; 2001-318749/34.

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or

PT diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

PS Claim 3; SEQ ID NO 6069; 2537pp + Sequence Listing; English.

XX The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises:

XX (a) an oligo-dT primer and an oligonucleotide complementary to the

XX complementary strand of a polynucleotide which comprises one of the 5602

XX oligonucleotide sequences defined in the specification, where the

XX complementary strand of a polynucleotide comprising a sequence complementary to the

XX complementary strand of a polynucleotide which comprises a 5'-end

XX sequence and an oligonucleotide comprising a sequence complementary to a

XX polynucleotide which comprises a 3'-end sequence, where the

XX oligonucleotide comprises at least 15 nucleotides and the combination of

XX the 5'-end sequence/3'-end sequence is selected from those defined in the

XX specification. The primer sets can be used in antisense therapy and in

XX gene therapy. The primers are useful for synthesizing polynucleotides,

CC particularly full-length cDNAs. The primers are also useful for the

CC detection and/or diagnosis of the abnormality of the proteins encoded by

CC the full-length cDNAs. The primers allow obtaining of the full-length

CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and

CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893

CC represent human amino acid sequences; and AAH13629 to AAH13632 represent

CC oligonucleotides, all of which are used in the exemplification of the

CC present invention

CC Sequence 579 BP; 139 A; 141 C; 114 G; 180 T; 0 U; 5 Other;

Query Match 8.5%; Score 74; DB 4; Length 579;
 Best Local Similarity 100.0%; Pred. No. 9.3e-18;

Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 268 CAGGCATGAGCCAC 281

RESULT 14
 AAH15304/C
 ID AAH15304 standard; cDNA; 1555 BP.

AC AAH15304;

DT 26-JUN-2001 (first entry)

DE Human cDNA sequence SEQ ID NO:13457.

KM Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

OS Homo sapiens.

PN EP1074617-A2.

PD 07-FEB-2001.

PF 28-JUL-2000; 2000EP-00116126.

PR 29-JUL-1999; 99JP-00248036.

PR 27-AUG-1999; 99JP-00300253.

PR 11-JAN-2000; 2000JP-00118776.

PR 02-MAY-2000; 2000JP-00183767.

PR 09-JUN-2000; 2000JP-00241899.

PA (HELI-) HELIX RES INST.

PI Ota T, Isegai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

DR WPI; 2001-318749/34.

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or

PT diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

PS Claim 6; SEQ ID NO 13457; 2537pp + Sequence Listing; English.

XX The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises:

XX (a) an oligo-dT primer and an oligonucleotide complementary to the

XX complementary strand of a polynucleotide which comprises one of the 5602

XX oligonucleotide sequences defined in the specification, where the

XX complementary strand of a polynucleotide comprising a sequence complementary to the

XX oligonucleotide comprises at least 15 nucleotides and the combination of

XX the 5'-end sequence/3'-end sequence is selected from those defined in the

XX specification. The primer sets can be used in antisense therapy and in

XX gene therapy. The primers are useful for synthesizing polynucleotides,

CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence and 3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialized methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
 CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 CC present invention

CC Sequence 1555 BP; 488 A; 296 C; 332 G; 439 T; 0 U; 0 Other;
 SQ

Query Match 8.5%; Score 74; DB 4; Length 1555;
 Best Local Similarity 100.0%; Pred. No. 7.7e-18;
 Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 TGGTCTCGAATCTCTGACCTGTGATCCGCCCGCTCGGCTCCCAAGTCTGGGATTA 119
 DB 1348 TGGTCTCGAATCTCTGACCTGTGATCCGCCCGCTCGGCTCCCAAGTCTGGGATTA 1289
 QY 120 CAGGATGAGCCAC 133
 DB 1288 CAGGATGAGCCAC 1275

RESULT 15
 ABR03562/c
 ID ABR03562 standard; cDNA; 139904 BP.
 XX
 AC ABR03562;
 DT 14-AUG-2002 (first entry)
 XX
 DE Human cDNA differentially expressed in granulocytic cells #133.
 XX
 XX Human; ss; granulocytic cell; DNA chip; bacterial infection;
 KM viral infection; parasitic infection; protozoal infection;
 KM fungal infection; sterile inflammatory disease; psoriasis;
 KM rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
 KM cardiac reperfusion injury; renal reperfusion injury; ARDS;
 KM adult respiratory distress syndrome; inflammatory bowel disease;
 KM Crohn's disease; ulcerative colitis; periodontal disease;
 KM granulocyte activation; chronic inflammation; allergy.
 XX
 OS Homo sapiens.
 XX
 XX WO200228999-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 03-OCT-2001; 2001WO-US030821.
 XX
 PR 03-OCT-2000; 2000US-0237189P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
 DR WPI; 2002-435328/46.
 XX
 XX
 PT Detecting granulocyte activation by detecting differential expression of
 CC genes associated with granulocyte activation, which serves as diagnostic
 PT markers that is useful for monitoring disease states and drug toxicity.
 XX
 PS Claim 1: SEQ ID NO 133, 114pp; English.
 CC
 CC The invention relates to detecting (M1) granulocyte (GC) activation
 CC (GCM), by detecting the level of expression of gene(s) (Gs) identified by
 CC DNA chip analysis as given in the specification, and comparing the

CC expression level to an expression level in an unactivated GC, where
 CC differential expression of Gs is indicative of GCM. Also included are
 CC modulating (M2) GA by contacting GC with an agent that alters the
 CC expression of at least one gene in Gs; (2) screening (M3) for an agent
 CC capable of modulating GCM or an inflammation (especially chronic) in a
 CC tissue, an allergic response in a subject, exposure of a subject to a
 CC pathogen or sterile inflammatory disease using the gene expression
 CC profile; (3) detecting (M4) an inflammation (especially chronic) in a
 CC tissue, an allergic response in a subject, exposure of a subject to a
 CC pathogen or sterile inflammatory disease, by detecting the level of
 CC expression in a sample of the tissue of gene(s) from Gs, where the level
 CC of expression of the gene is indicative of inflammation; (4) treating
 CC (M5) an inflammation (especially chronic) or in a tissue, an allergic
 CC response in a subject, exposure of a subject to a pathogen or sterile
 CC inflammatory disease, by contacting a tissue having inflammation with an
 CC agent that modulates the expression of gene(s) from Gs in the tissue. M1
 CC is useful for detecting GCM; M2 is useful for modulating GA; M3 is useful
 CC for screening an agent capable of modulating GCM preferably in an
 CC inflammation in a tissue; M4 is useful for detecting an inflammation
 CC (especially chronic) in a tissue, an allergic response in a subject,
 CC exposure of a subject to a pathogen or sterile inflammatory disease (e.g.
 CC psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,
 CC cardiac reperfusion injury, renal reperfusion injury, ARDS, adult
 CC respiratory distress syndrome, inflammatory bowel disease, Crohn's
 CC disease, ulcerative colitis, periodontal disease; also bacterial
 CC infection, viral infection, parasitic infection, protozoal infection,
 CC fungal infection and M5 is useful for treating one of the above
 CC conditions. The present sequence represents a gene differentially
 CC expressed in granulocytes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pat_sequences

CC Sequence 139904 BP; 39268 A; 29759 C; 30173 G; 40704 T; 0 U; 0 Other;
 SQ

Query Match 8.5%; Score 74; DB 6; Length 139904;
 Best Local Similarity 100.0%; Pred. No. 3.1e-18;
 Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 TGGTCTCGAATCTCTGACCTGTGATCCGCCCGCTCGGCTCCCAAGTCTGGGATTA 119
 DB 26820 TGGTCTCGAATCTCTGACCTGTGATCCGCCCGCTCGGCTCCCAAGTCTGGGATTA 26761
 QY 120 CAGGATGAGCCAC 133
 DB 26760 CAGGATGAGCCAC 26747

Search completed: May 24, 2004, 16:57:18
 Job time : 337 secs


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Db 121 AGGATGAGGCACTCGCCCAAGCCGCTCTTTTAAGATCCCGAGACTGACGCCAA 180
Qy 181 CCCATCTACTCTGATCTTTGGAACTCCCCCGACGCGCATTAATCTGACAGAGTA 240
Db 181 CCCATCTACTCTGATCTTTGGAACTCCCCCGACGCGCATTAATCTGACAGAGTA 240
Qy 241 AGACCAAGAGCAAGATGAGGAGTTCATCTAAGGTCGTGATGAGTGAAGAGAG 300
Db 241 AGACCAAGAGCAAGATGAGGAGTTCATCTAAGGTCGTGATGAGTGAAGAGAG 300
Qy 301 AAGATCAGCGAAACAAGCCTCTAGCTTTCTTACCAACAAGCCTCTGCCCCCT 360
Db 301 AAGATCAGCGAAACAAGCCTCTAGCTTTCTTACCAACAAGCCTCTGCCCCCT 360
Qy 361 GCTTTGAAAGGGGAGAGTATAGGGGAGCTGCCACCTGCTACAGTGAAGGAGTCT 420
Db 361 GCTTTGAAAGGGGAGAGTATAGGGGAGCTGCCACCTGCTACAGTGAAGGAGTCT 420
Qy 421 GGAGAATACTCACTTGTAGGTCTGCGCTCTTTCATCAGCCAGCTCTTAATAGCC 480
Db 421 GGAGAATACTCACTTGTAGGTCTGCGCTCTTTCATCAGCCAGCTCTTAATAGCC 480
Qy 481 AATGACCCCAAGGAGCTTACCAAGTCAAAAGAGCCCAATGCAATGATGAGAGAGG 540
Db 481 AATGACCCCAAGGAGCTTACCAAGTCAAAAGAGCCCAATGCAATGATGAGAGAGG 540
Qy 541 GAGGCAAAAGAGCTCGAGAGAGAGAGGAGCCCAATAGGCTGATTTCCAGTCCATA 600
Db 541 GAGGCAAAAGAGCTCGAGAGAGAGAGGAGCCCAATAGGCTGATTTCCAGTCCATA 600
Qy 601 GAGAGAGAGAGTGGGAGAGGAGGCTTTTGTATTAATGATCAATCTGTAATGCAAGTCA 660
Db 601 GAGAGAGAGAGTGGGAGAGGAGGCTTTTGTATTAATGATCAATCTGTAATGCAAGTCA 660
Qy 661 AATCCGGGATGCGGGTGAATGAGAGAGAGTCAACCTCGGGTGTCAATGGAGGCT 720
Db 661 AATCCGGGATGCGGGTGAATGAGAGAGAGTCAACCTCGGGTGTCAATGGAGGCT 720
Qy 721 CCAAGGCGGAGCTGCGCAAGAGAGATCGGCAAGAGGCTCTGAGCCAGCTCTGAGCCAA 780
Db 721 CCAAGGCGGAGCTGCGCAAGAGAGATCGGCAAGAGGCTCTGAGCCAGCTCTGAGCCAA 780
Qy 781 GCGACTCGGATTTGAACCCCGGCTCTCAAGGTGAGCTGTGAGCTTGAATGAATCAC 840
Db 781 GCGACTCGGATTTGAACCCCGGCTCTCAAGGTGAGCTGTGAGCTTGAATGAATCAC 840
Qy 841 TGCATGACCAATCTGTGCGGATTC 867
Db 841 TGCATGACCAATCTGTGCGGATTC 867

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RESULT 2
US-09-969-730-12
: Sequence 12, Application US/09969730
: Publication No. US2003005443A1
: GENERAL INFORMATION:
: APPLICANT: Ruben et al.
: TITLE OF INVENTION: 90 Human Secreted Proteins
: FILE REFERENCE: P2013P2
: CURRENT APPLICATION NUMBER: US/09/969,730
: CURRENT FILING DATE: 2001-10-04
: PRIOR APPLICATION NUMBER: 09/774,639
: PRIOR FILING DATE: 2001-02-01
: PRIOR APPLICATION NUMBER: 60/238,291
: PRIOR FILING DATE: 2000-10-06
: PRIOR APPLICATION NUMBER: 09/244,112
: PRIOR FILING DATE: 1999-02-04
: PRIOR APPLICATION NUMBER: PCT/US98/16235
: PRIOR FILING DATE: 1998-08-04
: PRIOR APPLICATION NUMBER: 60/056,371
: PRIOR FILING DATE: 1997-08-19
: PRIOR APPLICATION NUMBER: 60/056,732

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: PRIOR FILING DATE: 1997-08-19
: PRIOR APPLICATION NUMBER: 60/056,366
: PRIOR FILING DATE: 1997-08-19
: PRIOR APPLICATION NUMBER: 60/056,364
: PRIOR FILING DATE: 1997-08-19
: PRIOR APPLICATION NUMBER: 60/056,370
: PRIOR FILING DATE: 1997-08-19
: PRIOR APPLICATION NUMBER: 60/056,367
: PRIOR FILING DATE: 1997-08-19
: PRIOR APPLICATION NUMBER: 60/056,365
: PRIOR FILING DATE: 1997-08-19
: PRIOR APPLICATION NUMBER: 60/056,731
: PRIOR FILING DATE: 1997-08-19
: PRIOR APPLICATION NUMBER: 60/056,557
: PRIOR FILING DATE: 1997-08-19
: PRIOR APPLICATION NUMBER: 60/056,563
: PRIOR FILING DATE: 1997-08-19
: PRIOR APPLICATION NUMBER: 60/055,970
: PRIOR FILING DATE: 1997-08-18
: PRIOR APPLICATION NUMBER: 60/055,986
: PRIOR FILING DATE: 1997-08-18
: PRIOR APPLICATION NUMBER: 60/055,311
: PRIOR FILING DATE: 1997-08-05
: PRIOR APPLICATION NUMBER: 60/054,808
: PRIOR FILING DATE: 1997-08-05
: PRIOR APPLICATION NUMBER: 60/054,803
: PRIOR FILING DATE: 1997-08-05
: PRIOR APPLICATION NUMBER: 60/054,804
: PRIOR FILING DATE: 1997-08-05
: PRIOR APPLICATION NUMBER: 60/054,809
: PRIOR FILING DATE: 1997-08-05
: PRIOR APPLICATION NUMBER: 60/054,806
: PRIOR FILING DATE: 1997-08-05
: PRIOR APPLICATION NUMBER: 60/055,310
: PRIOR FILING DATE: 1997-08-05
: PRIOR APPLICATION NUMBER: 60/054,798
: PRIOR FILING DATE: 1997-08-05
: PRIOR APPLICATION NUMBER: 60/055,309
: PRIOR FILING DATE: 1997-08-05
: PRIOR APPLICATION NUMBER: 60/055,312
: PRIOR FILING DATE: 1997-08-05
: PRIOR APPLICATION NUMBER: 60/054,807
: PRIOR FILING DATE: 1997-08-05
: PRIOR APPLICATION NUMBER: 60/055,386
: PRIOR FILING DATE: 1997-08-05
: NUMBER OF SEQ ID NOS: 373
: SOFTWARE: Patencin Ver. 2.0
: SEQ ID NO 12
: LENGTH: 867
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (831)
: OTHER INFORMATION: n equals a,t,g, or c
US-09-969-730-12
Query Match 100.0%; Score 867; DB 10; Length 867;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCGAGTTTTTTTTTTTTTTTTTTTAAAGTAGAGAGGAGGTTTCAACCGTTAGCCAGGAT 60
Db 1 TCGAGTTTTTTTTTTTTTTTTTTTAAAGTAGAGAGGAGGTTTCAACCGTTAGCCAGGAT 60
Qy 61 GGTCTGAAGCTCTGACCTCGTATCGGCGCGCTCGGCTCCAAAGTGTGAGATTC 120
Db 61 GGTCTGAAGCTCTGACCTCGTATCGGCGCGCTCGGCTCCAAAGTGTGAGATTC 120
Qy 121 AGGATGAGGCACTGCGCCAGCGGCTTTTAAACATTTCCAGAGCTGTACGCCAA 180
Db 121 AGGATGAGGCACTGCGCCAGCGGCTTTTAAACATTTCCAGAGCTGTACGCCAA 180

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QY 181 CCCATCTGCTGACATTTGGGACTCCCCCGGCGCATTAAGTGTGAGAGTA 240
 Db 181 CCCATCTGCTGACATTTGGGACTCCCCCGGCGCATTAAGTGTGAGAGTA 240
 QY 241 AGACCAAGAGCAAGAAATGGGGATTCACATCTAAGTGTGATGATGATGAAGAA 300
 Db 241 AGACCAAGAGCAAGAAATGGGGATTCACATCTAAGTGTGATGATGATGAAGAA 300
 QY 301 AAGAAATGAGCAAAAGGCTCTAGTCTTTCTTACCAAAACCTCTCTGCCCACT 360
 Db 301 AAGAAATGAGCAAAAGGCTCTAGTCTTTCTTACCAAAACCTCTCTGCCCACT 360
 QY 361 GCTTTAAAGGGGAGAGATATGATGGGAGCTGCCACCTCTACAGAGAGGATCT 420
 Db 361 GCTTTAAAGGGGAGAGATATGATGGGAGCTGCCACCTCTACAGAGAGGATCT 420
 QY 421 GGAAGAAATCTCACTTTGAGGTCTGCTGCTCTTCTATCAGCAGCTCTTAAGCC 480
 Db 421 GGAAGAAATCTCACTTTGAGGTCTGCTGCTCTTCTATCAGCAGCTCTTAAGCC 480
 QY 481 AATGACCCCAAGGAGCTTACACAGTTCAAAAGGCCCAATGATGATGAGAGGG 540
 Db 481 AATGACCCCAAGGAGCTTACACAGTTCAAAAGGCCCAATGATGATGAGAGGG 540
 QY 541 GAGGCCAAAGACTCCGAGAGAGAGAGGCCCAATAAGCTGCTATTTCCGATCATA 600
 Db 541 GAGGCCAAAGACTCCGAGAGAGAGAGGCCCAATAAGCTGCTATTTCCGATCATA 600
 QY 601 GAGAGAGCAGAGTGGGAGAGGCTTTTGAATATGATATCTTGAATGCAAGTTCA 660
 Db 601 GAGAGAGCAGAGTGGGAGAGGCTTTTGAATATGATATCTTGAATGCAAGTTCA 660
 QY 661 AATCCGGGTATGCTGGGTGAGATATGAGAGCTTAACACTGGGTGATGAGAGCT 720
 Db 661 AATCCGGGTATGCTGGGTGAGATATGAGAGCTTAACACTGGGTGATGAGAGCT 720
 QY 721 CGAGGGCCGACTGGCCAGAGACATCGCAAGAGGCTCTGCAAGCCACTTGTGCGCA 780
 Db 721 CGAGGGCCGACTGGCCAGAGACATCGCAAGAGGCTCTGCAAGCCACTTGTGCGCA 780
 QY 781 GGCACGTGATTTGAACCCCGGCTCTCAAGGTAGCTGTAGCTTGANTGAACACC 840
 Db 781 GGCACGTGATTTGAACCCCGGCTCTCAAGGTAGCTGTAGCTTGANTGAACACC 840
 QY 841 TGCATATGACCAATCTGTCGCGAATTC 867
 Db 841 TGCATATGACCAATCTGTCGCGAATTC 867

RESULT 3
 US-10-621-363-12
 / Sequence 12, Application US/10621363
 / Publication No. US20040023283A1
 / GENERAL INFORMATION:
 / APPLICANT: Ruben et al.
 / TITLE OF INVENTION: 90 Human Secreted Proteins
 / FILE REFERENCE: P2013P2C1
 / CURRENT APPLICATION NUMBER: US/10/621,363
 / PRIOR FILING DATE: 2003-07-18
 / PRIOR APPLICATION NUMBER: 09/969,730
 / PRIOR FILING DATE: 2001-10-06
 / PRIOR APPLICATION NUMBER: 09/774,639
 / PRIOR FILING DATE: 2001-02-01
 / PRIOR APPLICATION NUMBER: 60/238,291
 / PRIOR FILING DATE: 2000-10-06
 / PRIOR APPLICATION NUMBER: 09/244,112
 / PRIOR FILING DATE: 1999-02-04
 / PRIOR APPLICATION NUMBER: PCT/US98/16235
 / PRIOR FILING DATE: 1998-08-04
 / PRIOR APPLICATION NUMBER: 60/056,371
 / PRIOR FILING DATE: 1997-08-19
 / PRIOR APPLICATION NUMBER: 60/056,732
 / PRIOR FILING DATE: 1997-08-19

/ PRIOR APPLICATION NUMBER: 60/056,366
 / PRIOR FILING DATE: 1997-08-19
 / PRIOR APPLICATION NUMBER: 60/056,364
 / PRIOR FILING DATE: 1997-08-19
 / PRIOR APPLICATION NUMBER: 60/056,370
 / PRIOR FILING DATE: 1997-08-19
 / Remaining Prior Application data removed - See file wrapper or PALM.
 / NUMBER OF SEQ ID NOS: 373
 / SOFTWARE: Patent In Ver. 2.0
 / SEQ ID NO 12
 / LENGTH: 867
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / FEATURES:
 / NAME/KEY: misc_feature
 / LOCATION: (831)
 / OTHER INFORMATION: n equals a,t,g, or c
 US-10-621-363-12

Query Match 100.0%; Score 867; DB 17; Length 867;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGAGTTTTTTTTTTTTTTTTTTTTTTTTTAAAGATGAGAGGAGTTTACCGTGTAGCCAGAT 60
 Db 1 TCGAGTTTTTTTTTTTTTTTTTTTTTTTTTAAAGATGAGAGGAGTTTACCGTGTAGCCAGAT 60
 QY 61 GGTCTCGAATCTCGACCTCGTGAATCCGCGCTCGGCTGCCAAATGCTGGGATAC 120
 Db 61 GGTCTCGAATCTCGACCTCGTGAATCCGCGCTCGGCTGCCAAATGCTGGGATAC 120
 QY 121 AGGCATGAGCAGCTGCGCCAGCGGCTTTTAAACATCCCGAGACTGACAGCAA 180
 Db 121 AGGCATGAGCAGCTGCGCCAGCGGCTTTTAAACATCCCGAGACTGACAGCAA 180
 QY 181 CCCATCTGACCTGACATTTGGGAACTCCCGCCAGCGCATTAAGTGTGAGAGTA 240
 Db 181 CCCATCTGACCTGACATTTGGGAACTCCCGCCAGCGCATTAAGTGTGAGAGTA 240
 QY 241 AGACCAAGAGCAAGAAATGGGGATTCACATCTAAGTGTGATGATGATGAAGAA 300
 Db 241 AGACCAAGAGCAAGAAATGGGGATTCACATCTAAGTGTGATGATGATGAAGAA 300
 QY 301 AAGAAATGAGCAAAAGGCTCTAGTCTTTCTTACCAAAACCTCTCTGCCCACT 360
 Db 301 AAGAAATGAGCAAAAGGCTCTAGTCTTTCTTACCAAAACCTCTCTGCCCACT 360
 QY 361 GCTTTAAAGGGGAGAGATATGATGGGAGCTGCCACCTCTACAGAGAGGATCT 420
 Db 361 GCTTTAAAGGGGAGAGATATGATGGGAGCTGCCACCTCTACAGAGAGGATCT 420
 QY 421 GGAAGAAATCTCACTTTGAGGTCTGCTGCTCTTCTATCAGCAGCTCTTAAGCC 480
 Db 421 GGAAGAAATCTCACTTTGAGGTCTGCTGCTCTTCTATCAGCAGCTCTTAAGCC 480
 QY 481 AATGACCCCAAGGAGCTTACACAGTTCAAAAGGCCCAATGATGATGAGAGGG 540
 Db 481 AATGACCCCAAGGAGCTTACACAGTTCAAAAGGCCCAATGATGATGAGAGGG 540
 QY 541 GAGGCCAAAGACTCCGAGAGAGAGAGGCCCAATAAGCTGCTATTTCCGATCATA 600
 Db 541 GAGGCCAAAGACTCCGAGAGAGAGAGGCCCAATAAGCTGCTATTTCCGATCATA 600
 QY 601 GAGAGAGCAGAGTGGGAGAGGCTTTTGAATATGATATCTTGAATGCAAGTTCA 660
 Db 601 GAGAGAGCAGAGTGGGAGAGGCTTTTGAATATGATATCTTGAATGCAAGTTCA 660
 QY 661 AATCCGGGTATGCTGGGTGAGATATGAGAGCTTAACACTGGGTGATGAGAGCT 720
 Db 661 AATCCGGGTATGCTGGGTGAGATATGAGAGCTTAACACTGGGTGATGAGAGCT 720
 QY 721 CGAGGGCCGACTGGCCAGAGACATCGCAAGAGGCTCTGCAAGCCACTTGTGCGCA 780

DB 721 CCAGGCGGACTGCGCAGAGACAGATCCGACAGAGCTCTGACGCTCTGATCCAA 780
QY 781 GCCATCGGATTTGAACCCCGGCTCTCTCAAGGTGAGCTGTGAGCTTGATGAAACAC 840
DB 781 GCCATCGGATTTGAACCCCGGCTCTCTCAAGGTGAGCTGTGAGCTTGATGAAACAC 840
QY 841 TCGTATGACCAATCTCTGTCGCGCAATTC 867
DB 841 TCGTATGACCAATCTCTGTCGCGCAATTC 867

RESULT 4
US-09-969-708-79/c
Sequence 79, Application US/09969708
Patent No. US20020102532A1
GENERAL INFORMATION:
APPLICANT: Augustus, Meena
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu

FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/969,708
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: US/60/237,606
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,608
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,425
PRIOR FILING DATE: 2000-10-03
SOFTWARE OF SEQ ID NOS: 658
SOFTWARE: PatentIn version 3.0
SEQ ID NO 79
LENGTH: 145831
TYPE: DNA
ORGANISM: Homo sapiens
US-09-969-708-79

Query Match 11.3%; Score 98; DB 9; Length 145831;
Best Local Similarity 100.0%; Pred. No. 5.2e-40;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 AGTAGAGATGGGCTTTACCGCTGTGACCGAGATGGTCTCGAATCTCGAATCTCTGATC 86
DB 38600 AGTAGAGATGGGCTTTACCGCTGTGACCGAGATGGTCTCGAATCTCGAATCTCTGATC 38541
QY 87 CGCCCGCTCGGCTCTCCCAAGTGGTGGATTACAGGC 124
DB 38540 CGCCCGCTCGGCTCTCCCAAGTGGTGGATTACAGGC 38503

RESULT 5
US-09-954-456-2116/c
Sequence 2116, Application US/09954456
Patent No. US20020115057A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711

PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2116
LENGTH: 145831
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-456-2116

Query Match 11.3%; Score 98; DB 9; Length 145831;
Best Local Similarity 100.0%; Pred. No. 5.2e-40;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 AGTAGAGATGGGCTTTACCGCTGTGACCGAGATGGTCTCGAATCTCTGATC 86
DB 38600 AGTAGAGATGGGCTTTACCGCTGTGACCGAGATGGTCTCGAATCTCTGATC 38541
QY 87 CGCCCGCTCGGCTCTCCCAAGTGGTGGATTACAGGC 124
DB 38540 CGCCCGCTCGGCTCTCCCAAGTGGTGGATTACAGGC 38503

RESULT 6
US-09-873-367C-646/c
Sequence 646, Application US/09873367C
Publication No. US20030165839A1
GENERAL INFORMATION:
APPLICANT: Soppet, Daniel
APPLICANT: Augustus, Gregory
APPLICANT: Ebner, Reinhard
APPLICANT: Carter, Kenneth
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using

FILE REFERENCE: 689290-64
CURRENT APPLICATION NUMBER: US/09/873,367C
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: U.S. 60/236,891
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: U.S. 60/236,842
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: U.S. 60/244,867
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: U.S. 60/245,084
PRIOR FILING DATE: 2000-11-01
NUMBER OF SEQ ID NOS: 1067
SOFTWARE: PatentIn version 3.0
SEQ ID NO 646
LENGTH: 145831
TYPE: DNA
ORGANISM: Homo sapiens
US-09-873-367C-646

Query Match 11.3%; Score 98; DB 10; Length 145831;
Best Local Similarity 100.0%; Pred. No. 5.2e-40;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 AGTAGAGATGGGCTTTACCGCTGTGACCGAGATGGTCTCGAATCTCTGATC 86
DB 38600 AGTAGAGATGGGCTTTACCGCTGTGACCGAGATGGTCTCGAATCTCTGATC 38541
QY 87 CGCCCGCTCGGCTCTCCCAAGTGGTGGATTACAGGC 124
DB 38540 CGCCCGCTCGGCTCTCCCAAGTGGTGGATTACAGGC 38503

RESULT 7

US-10-240-425-363/c
 ; Sequence 363, Application US/10240425
 ; Publication No. US20040033502A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Williams, Amanda
 ; APPLICANT: Boland, Joseph F.
 ; APPLICANT: Lord, Reginald V.
 ; APPLICANT: Alvarez, Chris
 ; APPLICANT: Wetzel, Jon C.
 ; APPLICANT: Scheff, Uwe
 ; APPLICANT: Vockley, Joseph G.
 ; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
 ; FILE REFERENCE: 44921-5026
 ; CURRENT APPLICATION NUMBER: US/10/240,425
 ; PRIOR FILING DATE: 2002-09-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/09847
 ; PRIOR FILING DATE: 2001-03-28
 ; PRIOR APPLICATION NUMBER: US 60/193,446
 ; PRIOR FILING DATE: 2000-03-31
 ; NUMBER OF SEQ ID NOS: 1588
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 363
 ; LENGTH: 145831
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: Genbank Accession No. US20040033502A1 AF001548
 US-10-240-425-363

Query Match 11.3%; Score 98; DB 13; Length 145831;
 Best Local Similarity 100.0%; Pred. No. 5,2e-40;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 AGTAGAGATGGGGTTTACCGGTGTAGCCAGATGATCTCCAGACCTCGTGGATCC 86
 DB 38600 AGTAGAGATGGGGTTTACCGGTGTAGCCAGATGATCTCCAGACCTCGTGGATCC 38541
 QY 87 CGCCCGCCTCGGCTCCCAAGTGTGAGATTACAGGC 124
 DB 38540 CGCCCGCCTCGGCTCCCAAGTGTGAGATTACAGGC 38503

RESULT 8
 US-09-860-670-196
 ; Sequence 196, Application US/09860670
 ; Patent No. US20020165137A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PA127P1
 ; CURRENT APPLICATION NUMBER: US/09/860,670
 ; PRIOR FILING DATE: 2001-05-21
 ; PRIOR APPLICATION data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 289
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 196
 ; LENGTH: 267
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-860-670-196

Query Match 8.7%; Score 75; DB 9; Length 267;
 Best Local Similarity 100.0%; Pred. No. 5,3e-28;
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 CTCCTGACCTGTGATCGCCGCTCGGCTCCCAAGTGTGAGATTACAGGATGAG 129
 DB 193 CTCCTGACCTGTGATCGCCGCTCGGCTCCCAAGTGTGAGATTACAGGATGAG 252
 QY 130 CCACTGGCCCAAGCC 144
 DB 253 CCACTGGCCCAAGCC 267

RESULT 9

US-10-227-646-196
 ; Sequence 196, Application US/10227646
 ; Publication No. US20030235829A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PA127P1
 ; CURRENT APPLICATION NUMBER: US/10/227,646
 ; PRIOR FILING DATE: 2002-08-26
 ; PRIOR APPLICATION NUMBER: US/09/860,670
 ; PRIOR FILING DATE: 2001-05-21
 ; PRIOR APPLICATION NUMBER: 60/205,515
 ; PRIOR FILING DATE: 2000-05-19
 ; NUMBER OF SEQ ID NOS: 289
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 196
 ; LENGTH: 267
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-227-646-196

Query Match 8.7%; Score 75; DB 16; Length 267;
 Best Local Similarity 100.0%; Pred. No. 5,3e-28;
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 CTCCTGACCTGTGATCGCCGCTCGGCTCCCAAGTGTGAGATTACAGGATGAG 129
 DB 193 CTCCTGACCTGTGATCGCCGCTCGGCTCCCAAGTGTGAGATTACAGGATGAG 252
 QY 130 CCACTGGCCCAAGCC 144
 DB 253 CCACTGGCCCAAGCC 267

RESULT 10
 US-09-867-701-10441/c
 ; Sequence 10441, Application US/09867701
 ; Patent No. US20020132237A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aglate, Paul A.
 ; APPLICANT: Jones, Robert
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.497
 ; CURRENT APPLICATION NUMBER: US/09/867,701
 ; PRIOR FILING DATE: 2001-05-29
 ; NUMBER OF SEQ ID NOS: 10912
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 10441
 ; LENGTH: 269
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-09-867-701-10441

Query Match 8.2%; Score 71; DB 9; Length 269;
 Best Local Similarity 100.0%; Pred. No. 6e-26;
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 TGACCTGTGATCGCCGCTCGGCTCCCAAGTGTGAGATTACAGGATGAGCCAC 133
 DB 163 TGACCTGTGATCGCCGCTCGGCTCCCAAGTGTGAGATTACAGGATGAGCCAC 104
 QY 134 TGCGCCCAAGCC 144
 DB 103 TGCGCCCAAGCC 93

RESULT 11
 US-10-027-632-249911/c

Fri May 28 12:50:56 2004

us-10-621-363-12.rmpb

Page 6

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; Sequence 249911, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 249911
; LENGTH: 548
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-249911
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Query Match      8.1%; Score 70; DB 13; Length 548;
Best Local Similarity 100.0%; Pred. No. 1.9e-25;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 CTCCTGACCTGCTGATCCGCGCCCTCGGCTCCCAAGTGTGGATTACAGGCATGAG 129
DB 548 CTCCTGACCTGCTGATCCGCGCCCTCGGCTCCCAAGTGTGGATTACAGGCATGAG 489
QY 130 CCACTGCGCC 139
DB 488 CCACTGCGCC 479
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RESULT 12
US-10-027-632-249911/c
; Sequence 249911, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 249911
; LENGTH: 548
```

```
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-249911

Query Match      8.1%; Score 70; DB 16; Length 548;
Best Local Similarity 100.0%; Pred. No. 1.9e-25;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 CTCCTGACCTGCTGATCCGCGCCCTCGGCTCCCAAGTGTGGATTACAGGCATGAG 129
DB 548 CTCCTGACCTGCTGATCCGCGCCCTCGGCTCCCAAGTGTGGATTACAGGCATGAG 489
QY 130 CCACTGCGCC 139
DB 488 CCACTGCGCC 479
```

```
RESULT 13
US-10-087-192-190
; Sequence 190, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 528452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 190
; LENGTH: 54200
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-087-192-190
```

```
Query Match      8.1%; Score 70; DB 13; Length 54200;
Best Local Similarity 100.0%; Pred. No. 1.4e-25;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 CTCCTGACCTGCTGATCCGCGCCCTCGGCTCCCAAGTGTGGATTACAGGCATGAG 129
DB 4549 CTCCTGACCTGCTGATCCGCGCCCTCGGCTCCCAAGTGTGGATTACAGGCATGAG 4608
QY 130 CCACTGCGCC 139
DB 4609 CCACTGCGCC 4618
```

```
RESULT 14
US-10-293-864-11/c
; Sequence 11, Application US/10293864
; Publication No. US20040092465A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF HUNTINGTIN INTERACTING PROTEIN 1 EXPRESSION
; FILE REFERENCE: RTS-0432
; CURRENT APPLICATION NUMBER: US/10/293,864
; PRIOR FILING DATE: 2002-11-11
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO: 11
; LENGTH: 65454
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-293-864-11

Query Match      8.1%; Score 70; DB 17; Length 65454;
```

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us-10-621-363-12.rmpb

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Best Local Similarity 100.0%; Pred. No. 1,3e-25;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 CTTGACCTGCTGATCCGCGCTCCGCGCTCCCAAGTGTGGGATTACAGGATGAG 129
DB 9836 CTTGACCTGCTGATCCGCGCTCCGCGCTCCCAAGTGTGGGATTACAGGATGAG 9777
QY 130 CCACTGCGCC 139
DB 9776 CCACTGCGCC 9767

RESULT 15
US-10-027-632-13366/c
; Sequence 13366, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO: 13366
; LENGTH: 748
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-13366

Query Match 7.8%; Score 68; DA 13; Length 748;
Best Local Similarity 100.0%; Pred. No. 2e-24;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 CTTGACCTGCTGATCCGCGCTCCGCGCTCCCAAGTGTGGGATTACAGGATGAGCC 131
DB 356 CTTGACCTGCTGATCCGCGCTCCGCGCTCCCAAGTGTGGGATTACAGGATGAGCC 297
QY 132 ACTGCGCC 139
DB 296 ACTGCGCC 289

Search completed: May 24, 2004, 18:26:31
Job time : 363 secs